

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 00:16:06 ; Search time 467 Seconds
(without alignments)
10599.341 Million cell updates/sec

Title: US-09-913-858a-1

Perfect score: 2198

Sequence: 1 actaactcaaacgcgcatt.....aaaaaaaaaaaaaaaaaa 2198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N.Geneseq_101002.*

- 1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
- 2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
- 6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
- 7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
- 8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
- 9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
- 10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
- 11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
- 12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
- 13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
- 14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
- 15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
- 16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
- 17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
- 18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query length	DB ID	Description
1	2198	100.0	2198	21	AAA97937
2	661.6	30.1	1982	21	AAC39529
3	209.4	9.5	2069	22	AAF84907
4	209.4	9.5	2124	22	AAF84910
5	209.4	9.5	2165	22	AAF84913
6	209.4	9.5	2232	22	AAF84916
7	209.4	9.5	2808	22	AAF84906
8	209.4	9.5	2863	22	AAF84909
9	209.4	9.5	2904	22	AAF84912

10	209.4	9.5	2971	22	AAF84915	Nitrogen-inducible
11	209.4	9.5	3714	22	AAF84905	Nitrogen-inducible
12	209.4	9.5	3775	22	AAD38881	Alfalfa AP2 adapto
13	105	4.8	105	21	AAA97938	Mung bean alpha 1,
14	84.2	3.8	287	21	ABL76406	Corn tassels-derive
15	50	2.3	1461	21	AAC40119	Arabidopsis thalia
16	49.2	2.2	676	22	AA541344	CDNA encoding nove
17	49.2	2.2	1328	24	ABK11711	DNA encoding novel
18	49.2	2.2	1479	24	ABA05334	Human fucosyltrans
19	49.2	2.2	2557	24	ABA05333	Human fucosyltrans
20	47.6	2.2	358	22	AAF64428	Human fucosyltrans
21	47	2.1	34769	22	AA546775	Novel human polynu
22	46.6	2.1	34769	22	AA546774	Tumour suppressor
23	46	2.1	5931	22	AA546703	Tumour suppressor
24	45.8	2.1	6136	24	ABK40042	Tumour suppressor
25	45	2.0	612	22	AAH71471	Human chemically p
26	44.8	2.0	9814	22	ABK31429	Human cervical can
27	44.2	2.0	10020	24	ABK34293	Signal transductio
28	44.2	2.0	12405	22	AA545330	Human immune syste
29	44.2	2.0	12405	24	AA561143	Chemically pretrea
30	44.2	2.0	12405	24	ABK28169	Human gene regulat
31	43.6	2.0	626	23	ABV60941	DNA transcription
32	43.6	2.0	2036	21	AA92672	Human prostate exp
33	43.6	2.0	2170	21	AA92645	Murine alpha-1,3-f
34	43.6	2.0	113515	24	ABL34175	Murine alpha-1,3-f
35	43.4	2.0	5857	24	AA563347	Human immune syste
36	43.2	2.0	2676	21	AA929647	Chemically pretrea
37	43.2	2.0	2822	21	AA929646	Human alpha-1,3-fu
38	43	2.0	10377	24	ABL34221	Human alpha-1,3-fu
39	42.6	1.9	9652	24	ABL32908	Human immune syste
40	42.4	1.9	1465	21	AAC40055	Human immune syste
41	42.4	1.9	1563	21	AAC41754	Arabidopsis thalia
42	42.2	1.9	626	23	ABV60941	Human prostate exp
43	41	1.9	1373	21	AACT7739	Human cancer assoc
44	41	1.9	4065	21	AAFI8226	Lung cancer assoc
45	41	1.9	5593	24	ABL33161	Human immune syste

ALIGNMENTS

RESULT 1
AAA97937 standard; DNA: 2198 BP.

AC AAA97937:

DT 26-JAN-2001 (first entry)

DE Mung bean alpha 1,3-fucosyltransferase DNA.

XX

KW alpha 1,3-fucosyltransferase; plant; mung bean; glycoprotein; insect;

KW GlcNAc-alpha1,3-fucosyl transferase; ds.

XX

OS Phaseolus aureus.

XX

PN WO200049153-A1.

XX

PD 24-AUG-2000.

XX

PF 17-FEB-2000; 2000WO-AT00040.

XX

PR 18-FEB-1999; 99AT-0000270.

XX

PA (ALTM/) ALTMANN F.

XX

PI Altman F;

XX

DR WPI: 2000-549274/50.

XX

PT P-PSDB; AAB10713.

XX

PT DNA encoding plant GlcNAc-alpha-1,3-fucosyl transferase; useful for recombinant production of the enzyme and recombinant glycoprotein

|||||
Db 1861 TCTGGCCAACTCATGTATGTTTGTATAGACATCACACTTATATTTAACTGTTTC 1920
Oy 1921 TGTGAAGTGCATTCATATTTAATGCTTGTAGTTTGTGCTTATCTGATCATCTGCA 1980
Db 1921 TGTGAAGTGCATTCATATTTAATGCTTGTAGTTTGTGCTTATCTGATCATCTGCA 1980
Oy 1981 AGTCACATCTCTTATATTTGATGAGTGAACATAATCTATATGAGAGATCATGTTT 2040
Db 1981 AGTCACATCTCTTATATTTGATGAGTGAACATAATCTATATGAGAGATCATGTTT 2040
Oy 2041 CACTCAAGACACATTTACTTACTCATGTTGTTTGAATGATCGAGCTTTTGTAGTCTG 2100
Db 2101 GAACTGCCCTGTGTTGACACCTGTTATGCTTCTGATGATCGAGCTTTTGTAGTCTG 2160
Oy 2161 GAACTGCCCTGTGTTGACACCTGTTATGCTTCTGATGATCGAGCTTTTGTAGTCTG 2160
Db 2161 GAACTGCCCTGTGTTGACACCTGTTATGCTTCTGATGATCGAGCTTTTGTAGTCTG 2160
Oy 2161 GTTTGTGACCTCTAATAAAAAAAAAAAAAAAAAAAAAA 2198
Db 2161 GTTTGTGACCTCTAATAAAAAAAAAAAAAAAAAAAAAA 2198
RESULT 2
AAC39529
ID AAC39529 standard; DNA; 1982 BP.
AC AAC39529;
XX
XX 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 24967.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136782.
PR 28-MAY-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.

PR	27-JUL-1999;	99US-0145919;	PR	26-OCT-1999;	99US-0161359;
PR	28-JUL-1999;	99US-0145951;	PR	26-OCT-1999;	99US-0161360;
PR	02-AUG-1999;	99US-0146386;	PR	26-OCT-1999;	99US-0161361;
PR	02-AUG-1999;	99US-0146388;	PR	28-OCT-1999;	99US-0161920;
PR	02-AUG-1999;	99US-0146389;	PR	28-OCT-1999;	99US-0161922;
PR	03-AUG-1999;	99US-0147038;	PR	28-OCT-1999;	99US-0161993;
PR	04-AUG-1999;	99US-0147204;	PR	29-OCT-1999;	99US-0162142;
PR	04-AUG-1999;	99US-0147302;			
PR	05-AUG-1999;	99US-0147192;			
PR	05-AUG-1999;	99US-0147260;			
PR	06-AUG-1999;	99US-0147303;			
PR	06-AUG-1999;	99US-0147416;			
PR	09-AUG-1999;	99US-0147493;			
PR	09-AUG-1999;	99US-0147935;			
PR	10-AUG-1999;	99US-0148171;			
PR	11-AUG-1999;	99US-0148319;			
PR	12-AUG-1999;	99US-0148341;			
PR	13-AUG-1999;	99US-0148365;			
PR	13-AUG-1999;	99US-0148684;			
PR	16-AUG-1999;	99US-0149368;			
PR	17-AUG-1999;	99US-0149175;			
PR	18-AUG-1999;	99US-0149426;			
PR	20-AUG-1999;	99US-0149722;			
PR	20-AUG-1999;	99US-0149723;			
PR	20-AUG-1999;	99US-0149929;			
PR	23-AUG-1999;	99US-0149902;			
PR	23-AUG-1999;	99US-0149930;			
PR	25-AUG-1999;	99US-0150566;			
PR	26-AUG-1999;	99US-0150884;			
PR	27-AUG-1999;	99US-0151065;			
PR	27-AUG-1999;	99US-0151066;			
PR	27-AUG-1999;	99US-0151080;			
PR	30-AUG-1999;	99US-0151303;			
PR	31-AUG-1999;	99US-0151348;			
PR	01-SEP-1999;	99US-0151930;			
PR	07-SEP-1999;	99US-0152363;			
PR	10-SEP-1999;	99US-0153070;			
PR	13-SEP-1999;	99US-0153758;			
PR	13-SEP-1999;	99US-0154018;			
PR	16-SEP-1999;	99US-0154039;			
PR	20-SEP-1999;	99US-0154779;			
PR	22-SEP-1999;	99US-0155139;			
PR	23-SEP-1999;	99US-0155486;			
PR	24-SEP-1999;	99US-0155659;			
PR	28-SEP-1999;	99US-0156458;			
PR	29-SEP-1999;	99US-0156596;			
PR	04-OCT-1999;	99US-0157117;			
PR	05-OCT-1999;	99US-0157753;			
PR	06-OCT-1999;	99US-0157865;			
PR	07-OCT-1999;	99US-0158020;			
PR	08-OCT-1999;	99US-0158232;			
PR	12-OCT-1999;	99US-0158369;			
PR	13-OCT-1999;	99US-0159293;			
PR	13-OCT-1999;	99US-0159294;			
PR	13-OCT-1999;	99US-0159295;			
PR	14-OCT-1999;	99US-0159329;			
PR	14-OCT-1999;	99US-0159330;			
PR	14-OCT-1999;	99US-0159331;			
PR	14-OCT-1999;	99US-0159637;			
PR	14-OCT-1999;	99US-0159638;			
PR	18-OCT-1999;	99US-0159584;			
PR	21-OCT-1999;	99US-0160741;			
PR	21-OCT-1999;	99US-0160767;			
PR	21-OCT-1999;	99US-0160778;			
PR	21-OCT-1999;	99US-0160780;			
PR	21-OCT-1999;	99US-0160770;			
PR	21-OCT-1999;	99US-0160814;			
PR	21-OCT-1999;	99US-0160815;			
PR	22-OCT-1999;	99US-0160980;			
PR	22-OCT-1999;	99US-0160981;			
PR	22-OCT-1999;	99US-0160989;			
PR	25-OCT-1999;	99US-0161404;			
PR	25-OCT-1999;	99US-0161405;			
PR	25-OCT-1999;	99US-0161406;			

PR	26-OCT-1999;	99US-0161359;	PR	26-OCT-1999;	99US-0161359;
----	--------------	---------------	----	--------------	---------------

Db	1155	GCACGTTTGAAGAGATGAAAGTATCTGCGAGCTAACCCCTGCGTATTAAATACACACT	1214
Oy	1257	GAGGTGCAAGTATGAGGGTTCATCTGACTCTTCAAGGCCCTTGATATGACAGTCT	1318
Db	1215	AAGATGGAAATACGAGGGTCCCTTCAGATTCCTTTCAGAGGCATTTGTAATGCTGCTGT	1274
Oy	1317	GCATTCATCGGCGCTTTTGCACTTCACTGGCCACAGTGAAGAGAGAGAGAGAA	1376
Db	1275	ACACTCTTCTTGCGCTCTCTGCAATTTTCCCTGCGCCACGAGGGTCCGAGACAGAAAGAGGA	1334
Oy	1377	TAAATCAAGCCCTTAAGAGACGCTCTTGCAAGT--GCACTAGAGGGCCAGAAACCGTATA	1433
Db	1335	AAGCCCTAAATTCAGAGAAACGACCGTGCAGAAATGTAGCAGGGGAGATCAGACACAGTTTA	1394
Oy	1434	TCATATCTATGTGAGAAAGGGGAAAGGTTTGATGATGAGTCCATTTTACCTAGAGTCTAG	1493
Db	1395	TCATGTTTTTTGTTAGAAAGAGGCGCGGTTTGAATGGAATAGTCTTTTGTAGGGGTAA	1454
Oy	1494	CAATTTACTCTGAAATCTGTGAGAGCTGCTGTTGTTGAAGTTCACATCCCTGAATCT	1553
Db	1455	AAGTGTGATCAGGAAGACCTCTAAATCTGTAAGTCTTCGCGCAAGTTCAAGTCTTTAAACA	1514
Oy	1554	TGTGCTCTGTATGAGACGCTGAAGGCCCTGAAGTTATAGAGGGGAGTGTCTTAAACT	1613
Db	1515	TGAGGCGAGTGTGGAAGAGGAAAGGCGCTGGAACCTTAAAGAGACAAAGAGACTTAAAT	1574
Oy	1614	CTAATAAATATACCAATTTGGCTTGACACAGACAGCAAGCTTTTAACTTCAGCTGCA	1673
Db	1575	ACATTCGATTTTACCCCGCTTGCGCTTAACGACAGACAGCGCTTTGTACAACTTAAATTCGA	1634
Oy	1674	AGGTGATGCTGATTTTCAGAGATCACTTGGAGAAACAATCCTTGTCCTCAAGTTTGAAGTAT	1733
Db	1635	GGGAAATTCGAGTCAAGTATGATGATCAATTCAAAACAACCTTGCTTAATTTGAGAGTTGT	1694
Oy	1734	TTTTGTGTAG 1743	
Db	1695	CTTGCTCTAG 1704	
RESULT 3			
AAF84907			
ID	AAF84907 standard; DNA: 2069 BP.		
AC	AAF84907:		
XX			
DT	09-JUL-2001 (first entry)		
DE	Nitrogen-Inducible promoter for regulating foreign gene expression.		
XX			
KM	nitrogen-inducible promoter; nitrile reductase gene; Nlr gene;		
XX	transgenic plant; transgene expression; ss.		
OS	Synthetic.		
PN	WO200125454-A2.		
XX			
PD	12-APR-2001.		
XX			
PF	02-OCT-2000; 2000WO-CA01143.		
XX			
PR	04-OCT-1999; 99US-0157133.		
XX			
PA	(MEDI-) MEDICAGO INC.		
XX			
PI	Vezina L, D'Aoust M;		
XX			
DR	WPI; 2001-308228/32.		
XX			
PT	Regulating foreign gene transcription in transgenic plants, comprises		
PT	transforming a plant (cell) with an expression construct having		
PT	nitrogen-inducible promoter, an open reading frame of a gene and a		
PT	polyadenylation site		

PS Claim 1, Page 30-31, 44pp; English.

CC AAF84905-17 represent nitrogen-inducible promoters. They are promoters
CC of the nitrite reductase (Nir) gene. The promoter is used for regulating
CC foreign gene transcription in transgenic organisms. The method uses an
CC expression construct having a nitrogen-inducible promoter, without
CC cis-acting sequence, operably linked to the gene to be expressed and
CC modulated for transcriptional expression of the gene by addition or
CC removal of a nitrogen inducer, an open reading frame of a gene, and a
CC 3' polyadenylation signal. The method is useful for regulating the
CC transcription of transgenes in genetically modified organisms. The
CC nitrogen-inducible expression cassettes are useful for the controlling
CC expression of foreign genes in plants.

XX Sequence 2069 BP; 640 A; 389 C; 335 G; 705 T; 0 other:

XX

XX Query Match 9.5%; Score 209.4; DB 22; Length 2069;
XX Best Local Similarity 66.5%; Pred. No. 2.5e-45;
XX Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2.

CC 1486 AGGCTAGCAATTTACTCTGATGCTGTGAGAGCGCTGCTGTGTTTGAAGTTCACATCC 1545
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 170 AGATTACCAATTTTACCTCGGAGCTGACAGCTGCTGTTCTTAACGATTCACGCTC 229
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 1546 CTGAATCTTGTCCTGTATGAGACAGACTGAAGAGCCTGAAGTATATAAGAGGGGAGTGT 1605
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 230 CTGATTCATGTCCTGATATGGAAGGCTGAAGACCTCAAAATTTCTAAAGGTGGCATAA 289
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 1606 TTAAACTCTACAAAATATACCAATTGGCTTGACACAGACAGAGCTCTTATACCTTC 1665
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 230 TTGAAGGTTTACAAAATATACCTTCGGGCTTGACACAGAGCAAGCTCTTATACCTTC 349
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 1666 AGCTTCAAAAGGTAGCTGATTTACAGAGTCACTTGGAGAACATTCCTGTGCCAAGTTT 1725
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 350 CAGTTCACAGGGGAGTGTGATTTTCAGAAAGTCACTTGGAGAGCAATCCTGTGCCAAGTTT 409
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 1726 GAGTCATTTTTTGTGTAGCATGCGCTAA-----ATGCTACCTCTGCTTACCTGATTT 1778
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 410 GAAGTAATTTTTTGTGTAGCATATGTTGAGCTACTTACAAATTTATCATGATGACCTGACATT 469
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 1779 ACCTTCACCTACTGAGCAGCTAGTAGAGTTTATAGGAATGAGTATGGCCAGTAATATGGC 1838
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 470 AGCTCTTTCACTTAACTGACAGATGAACTTTTGAAGAAATGATGACCATGAGTCGCGC 529
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 1839 ATGGCTT-----TATTATGCTCTAGTTCCTTGGCCAACACTGATGATGTTT 1884
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 530 ATGGCTTGTGATATGCTACCTACTCTTGGCCAACATCATGCGGGAATTTACATTACAGAAAT 589
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 1885 GTATATAGACATACACACTTAAATTTTAAACTGTGTTCTGTAGAAAGTGCACAAATCCATATTTA 1944
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 590 ATTCATATGATCAACCACTTAACCCCTTTTGTATAGATATACGAATGTTTCATATATTA 649
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 1945 ATGCTTAGTGTAGTGCCTCTATTCAGATCATCT 1977
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 650 ATGTTGGGTGTAGTGTCTTTTACTTGATATAT 682
CC | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX

XX RESULT 4
XX ID AAF84910
XX AAF84910 standard; DNA; 2124 BP.
XX
XX AAF84910;
XX
XX 09-JUL-2001 (first entry)
XX
XX Nitrogen-inducible promoter for regulating foreign gene expression.
XX
XX Nitrogen-inducible promoter; nitrite reductase gene; Nir gene;
XX transgenic plant; transgene expression; ss.
XX
XX Synthetic.
XX

RESULT 9

AAf84912 standard; DNA; 2904 BP.

AAf84912;

09-JUL-2001 (first entry)

Nitrogen-inducible promoter for regulating foreign gene expression.

nitrogen-inducible promoter; nitrile reductase gene; NIR gene;

transgenic plant; transgene expression; ss.

Synthetic.

WO200125454-A2.

12-APR-2001.

02-OCT-2000; 2000WO-CA01143.

04-OCT-1999; 99US-0157133.

(MEDI-) MEDICAGO INC.

Vezina L, D'Aoust M;

WPI; 2001-308228/32.

Regulating foreign gene transcription in transgenic plants, comprises transforming a plant (cell) with an expression construct having a nitrogen-inducible promoter, an open reading frame of a gene and a polyadenylation site.

Claim 1; Page 34-35; 44pp; English.

AAf84905-17 represent nitrogen-inducible promoters. They are promoters of the nitrile reductase (NIR) gene. The promoter is used for regulating foreign gene transcription in transgenic organisms. The method uses an expression construct having a nitrogen-inducible promoter, with(out) cis-acting sequence, operably linked to the gene to be expressed and modulated for transcriptional expression of the gene by addition or removal of a nitrogen inducer, an open reading frame of a gene, and a 3' polyadenylation signal. The method is useful for regulating the transcription of transgenes in genetically modified organisms. The CC nitrogen-inducible expression cassettes are useful for the controlling expression of foreign genes in plants.

Sequence 2904 BP; 903 A; 537 C; 491 G; 973 T; 0 other;

Query Match 9.5%; Score 209.4; DB 22; Length 2904;

Best Local Similarity 66.5%; Pred. No. 2.9e-45;

Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

QY 1486 AGGCTAGCAATTTAACTCTGAATGCTGTAAGGCTGCTGTTTGAAGTCCATCC 1545
 DB 909 AGATCTAGCAATTTAACTCTGAGATCTTCAAGACTGCTGTTCTTACGAAGTTACGTC 968
 QY 1546 CTGATCTTGGCTGTATGAGAGACTGAAGGCTGAAGTAAATGAAGGGGAGTGTCT 1605
 DB 969 CTGATCTTGGCTGTATGAGAGACTGAAGGCTGAAGTAAATGAAGGGGAGTGTCT 1028
 QY 1606 TTTAAACTTACAAATATATCCCAATTTGCTTGACACAGACAGCTTTTATACCTTC 1665
 DB 1029 TTGAAGTTTACAAATATATCCCTGCGGCTTGACACAGAGCAAGCTTTTATACCTTC 1088
 QY 1666 AGCTTCAAAAGTGATGCTGTTTCAGAGACACTGTTGAGAGCAATCTTGGCAATTT 1725
 DB 1089 CAGTTCAACGGGAGTGTGATTTTCAGAGTCACTTGAGAGCAATCTTGGCCAAATTT 1148
 QY 1726 GAAGTATTTTGTGTAGCATGCGCTAA-----ATGTTACCTCTGCTTACCTGAAT 1778

RESULT 10

AAf84915 standard; DNA; 2971 BP.

AAf84915;

09-JUL-2001 (first entry)

Nitrogen-inducible promoter for regulating foreign gene expression.

nitrogen-inducible promoter; nitrile reductase gene; NIR gene;

transgenic plant; transgene expression; ss.

Synthetic.

WO200125454-A2.

12-APR-2001.

02-OCT-2000; 2000WO-CA01143.

04-OCT-1999; 99US-0157133.

(MEDI-) MEDICAGO INC.

Vezina L, D'Aoust M;

WPI; 2001-308228/32.

Regulating foreign gene transcription in transgenic plants, comprises transforming a plant (cell) with an expression construct having a nitrogen-inducible promoter, an open reading frame of a gene and a polyadenylation site.

Claim 1; Page 36-37; 44pp; English.

AAf84905-17 represent nitrogen-inducible promoters. They are promoters of the nitrile reductase (NIR) gene. The promoter is used for regulating foreign gene transcription in transgenic organisms. The method uses an expression construct having a nitrogen-inducible promoter, with(out) cis-acting sequence, operably linked to the gene to be expressed and modulated for transcriptional expression of the gene by addition or removal of a nitrogen inducer, an open reading frame of a gene, and a 3' polyadenylation signal. The method is useful for regulating the transcription of transgenes in genetically modified organisms. The CC nitrogen-inducible expression cassettes are useful for the controlling expression of foreign genes in plants.

Sequence 2971 BP; 925 A; 549 C; 508 G; 989 T; 0 other;

Query Match 9.5%; Score 209.4; DB 22; Length 2971;

Best Local Similarity 66.5%; Pred. No. 3e-45; Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

DB 1149 GAAGTATTTTGTGTAGCATATGTGAGCTACCTCAATTTACATGATCACCAGCAT 1208
 QY 1779 AGCTTCACTTAGCTGAGCACTAGCTAGAGTTTATAGAAATGATGCGATATGCG 1838
 DB 1209 AGCTTTCACCTTAACGAGAGATGATTTTATAGAAATGATGCGATATGCG 1268
 QY 1839 ATGCGCTT-----TATTTAVGCCATGTTCTTGCCCACTCATTTGATGTTT 1884
 DB 1269 ATGCGCTTGTAAATGCCATACCTTCTTGCCCACTCATTTGATGATTTA 1328
 QY 1885 GTATTAACATCAACACTTTAATTTTAACTTGTGTAGAGTGCATAATTCATTTA 1944
 DB 1329 ATACATGACTTCAACCACTTAAACCCCTTTTGTAAAGATTAAGTAAATGTCATATTTA 1388
 QY 1945 ATGCTTATGTTTATGCTCTTATCTGATCATCT 1977
 DB 1389 ATGTTGGTGTGTAGTGTATTACTTGAATTAAT 1421

PD	10-MAY-2002.
XX	
PF	31-OCT-2001: 2001MO-CA01532.
XX	
PR	31-OCT-2000: 2000DS-244214P.
XX	
PA	(MED1-) MEDICAGO INC.
XX	
PI	Veziina L, D'acoust M, Arcand F, Bllodeau P;
DR	WPI: 2002-471503/50.
XX	
PT	Isolating and characterizing an expression regulatory sequence for
PT	expressing recombinant polypeptides and/or RNA, comprises producing
PT	oligonucleotide primers that amplify sequences upstream or downstream
XX	of cDNAs
XX	-
PS	
XX	Example 2; Page 67-68; 74pp; English.
CC	
CC	The invention relates to a method for isolating and characterising an
CC	expression regulatory sequence for the expression of recombinant
CC	polypeptides and/or RNA. The method comprising producing at least one
CC	oligonucleotide primer from cDNAs of a cDNA library, where the
CC	oligonucleotide primer allows amplification of genomic sequences upstream
CC	or downstream of the cDNAs. The method is useful for isolating,
CC	characterising and identifying a large number of known and unknown
CC	promoters that are active under any desired environmental condition to
CC	which a cell may be exposed and not just to the exemplified isolation of
CC	promoters that are capable of expression in specific conditions. The
CC	methods are also useful for cloning genes from any host, or from a
CC	specific tissue with such host, from which a cDNA library may be
CC	constructed; for the identification and isolation of analogous promoters,
CC	signal peptides and structural genes in several species of multicellular
CC	and unicellular organisms and as a high throughput identification system
CC	of candidate therapeutic targets. The promoter sequences may be used to
CC	regulate the synthesis of polypeptides. The present sequence is at least a
CC	AP2 adapter with nitrite reductase gene (Nir).
XX	
SO	Sequence 3775 BP; 1180 A; 658 C; 670 G; 1267 T; 0 other;

Query Match	9.5%	Score 209.4	DB 24	Length 3775
Best Local Similarity	66.5%	Pred. No. 3.3e-45		
Matches 341	Conservative 0	Mismatches 151	Indels 21	Gaps 2
QY 1486	AGGCTACCAATTACTCTGATGATGCTGGAAGGCTGCTGTTGTAAGTTCACATCC	1545		
Db 957	AGATTACCAATTAACTCTGGAGCTTTCAGACTGCTGTTTACGAAATTCACGCTCC	1016		
QY 1546	CTGATCTTGCGCCGTATMGAAAGCTGAAGCCTGAAGTTATTAAGAGGGGGAGTGT	1605		
Db 1017	CTGAATCATAGTTCGTATMGAAAGCTGAAGACCTCAAAATTCATAAGGTGGCATAAA	1076		
QY 1606	TTAAACTCTACAAATATATATACCAATTTGGCTGACACAGAGACAAGCTTTATACCTTC	1665		
Db 1077	TTGAAGGTTTACAAATATATATACCTTCGGGGCTTGACACAGAGCAAGCTTTATACCTTC	1136		
QY 1666	AGCTTCAAAAGGTGATGCTGATTTTACGAGAGTCACTTGAGAACATATCTTGTCCTCAAGTTT	1725		
Db 1137	CAGTTCACAGGGGAGTGTGATTTTCAGAAAGTCACTTGAGAGAGCAATCTTGTCCTCAAGTTT	1196		
QY 1726	GAAGTCATTTTGTGTATGACATGCGCTAA-----ATGGTACCTCGCTCTACCTGAAT	1778		
Db 1197	GAGTAATTTTTGTGTATGACATATGTTGAGACATACCTCAATTTACATGATCACTTACGAT	1256		
QY 1779	AGCTTCACTTACCTGAGCAGCACTAGTAGTATTAGCAATGAGTATGCGCAATATAGGC	1838		
Db 1257	AGCTTTCACCTTACTAGCAGAGAAATGAAGTTTATAGCAATGAGTATGACCATGAGCTCGGC	1316		
QY 1839	ATGCGTT-----TATTATAGCCAGATTTCTTGCCCAACATCATGATGATGTTT	1884		
Db 1317	ATGCGTTTGTATAGCTTACCTACCTACTTTGGCCCAACTCATCGGGGATTTTACATTCACAGAAAT	1376		
QY 1885	GTATATGACATCACACTTAAATTTTAAACTGTGTTCTGTAGAAAGTGCAAATTCATATTTTA	1944		

Db 1377 ATAAATACCTTCACACCTACTTAAACCCCTTTTGTGAATACTGATGATCATATTTA 1436

Qy 1945 ATGCTAGTTTATAGTGCCTTATCATGATCATCH 1977

Db 1437 ATGTGGGTTGTACTGTTTACTTGATATATA 1469

RESULT 13
AAA97938
ID AAA97938 standard; DNA; 105 BP.

AC	AAA97938;
XX	
DT	26-JAN-2001 (first entry)
XX	

Mung bean alpha 1,3-fucosyltransferase DNA fragment

KM alpha 1,3-fucosyltransferase; plant; mung bean; glycoprotein; insect
KM GlcNAc-alpha1,3-fucosyl transferase; ds.

XX W0200049153-A1
PN
UN

PD 24-AUG-2000.

PF 17-FEB-2000; 2000WO-AT000040.

PR 18-FEB-1999; 99AT-0000270.

PA (ALTM/) ALTMANN F.

PI Altmann F;

DR WPI; 2000-549274/50

XX
DE
CUTS
to
the
7th
of
the
1st

PT recombinant production of the enzyme and recombinant glycoprotein

X

XX
XX
E

This invention describes a novel DNA molecule (I), encoding a plant protein with fucosyl transferase activity, GlcNAc- α -1,3-fucosyl transferase. The methods and DNA sequences are useful for production of recombinant GlcNAc- α -1,3-fucosyltransferase. The enzyme is useful for the production of recombinant human glycoproteins, which are especially useful in medical applications and pharmaceutical compositions. (I) can be used as a probe to select GlcNAc- α -1,3-fucosyltransferase coding sequences in a sample, especially from plants or insects. This sequence encodes a fragment of the mung bean (*Phaseolus aureus*) α 1,3-fucosyltransferase protein described in the method of the invention.

Sequence 105 BP; 33 A; 21 C; 20 G; 31 T; 0 other;

Query Match	4.8%	Score 105	DB 21	Length 105
Best Local Similarity	100.0%	Pred. No.	4.4e-18	
Matches 105	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0

[illegible]

QY 1069 GTAAC TGA A A A T T C T T C C A T C C C T G T G C T G G A A C T G T C C C T 1113

Db 61 G T A A C T G A A A A A T T C T T C C A A T C C C T T G T T G C T G G A A C T G T C C C T 105

ID	ABL76406 standard; cDNA; 287 BP.
XX	
AC	ABL76406;
XX	
DT	14-MAY-2002 (first entry)
XX	
DE	Corn tassal-derived polynucleotide (cdps) SEQ ID NO:5780.
XX	
KW	Corn; corn tassal-derived polynucleotide; cdps; hybrid breeding; CDPS;
KW	inheritance; characteristic; growth; development; disease resistance;
KW	environmental adaptability; quality; yield; molecular marker;
KW	multigene trait; plant breeding; corn tassal; gene; ss.
XX	
OS	Zea mays.
XX	
PN	US2001051335-A1.
XX	
PD	13-DEC-2001.
XX	
PF	16-APR-1999; 99US-0294093.
XX	
PR	21-APR-1998; 98US-082567P.
XX	
PA	(LALG/) LALGUDI R V.
XX	(ITOL/) ITO L Y.
PA	(SHER/) SHERMAN B K.
XX	
PI	Lalguudi RV, Ito LY, Sherman BK;
XX	
DR	WPI: 2002-163647/21.
XX	
PT	Novel purified corn tassal-derived polynucleotide useful for
PT	determining altered gene expression, to recover regulatory elements and
PT	to follow inheritance of desirable characteristics through hybrid
PT	breeding programs -
XX	
XX	Claim 1; SEQ ID 5780; 201pp; English.
XX	
CC	The present sequence describes a purified corn tassal-derived
CC	polynucleotide sequence (cdps) comprising a nucleic acid sequence
CC	selected from those given in ABL70627 to ABL76833. The cdps sequences
CC	encode corn tassal-derived polypeptides (CDPS). The cdps sequences (I)
CC	can be used for determining altered gene expression, to recover
CC	regulatory elements and to follow inheritance of desirable
CC	characteristics through hybrid breeding programs. (I) are also useful
CC	in the evaluation, and alteration of desired characteristics associated
CC	with growth and development, disease resistance, environmental
CC	adaptability, quality and yield, and as molecular markers for studying
CC	inheritance of multigene traits in a plant breeding program. (I) can be
CC	used to produce a tassal-specific profile of gene transcription, a
CC	transcript image, to clone regulatory elements for use in transformation
CC	vectors, to express a polypeptide, to identify, isolate or extend
CC	identical or related corn tassal nucleic acid sequences from DNA
CC	libraries, in nucleic acid hybridisation or amplification technologies,
CC	as for query sequences to determine homology of known sequences, as probe
CC	for use in Southern or Northern hybridisation, and to identify the
CC	presence of and/or to determine the degree of similarity between two
CC	(or more) nucleic acid sequences.
XX	
XX	Sequence 287 BP; 78 A; 57 C; 62 G; 90 T; 0 other;
XX	
QY	Query Match 3.8%; Score 84.2; DB 24; Length 287;
	Best Local Similarity 67.2%; Pred. No. 2.5e-12;
DB	Matches 119; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
XX	
QY	658 GCATTGGGTAACCTCAACCAAGTGAACAGCTAGCAATTCGATCAATGGAATCAGCA 717
	1 1
DB	39 GGACTGGGTAATCTCTCTCTGTGAGGGGTATCTCGATCAATGGAATCAATCT 98
	1 1
QY	718 GAATCATCTAGCGAGAACAAATTTCCATTCGGAACAGGAGGAGATATTAATCTGTAAG 777
	1 1
DB	99 CAATATTTATCAAGAAATAGTATGTGATGCTCGAGGAGAGGGGTACCAAGATTTGATG 158

[illegible]

```

PR 18-JUN-1999; 9905-0139454.
PR 18-JUN-1999; 9905-0139455.
PR 18-JUN-1999; 9905-0139456.
PR 18-JUN-1999; 9905-0139457.
PR 18-JUN-1999; 9905-0139458.
PR 18-JUN-1999; 9905-0139459.
PR 18-JUN-1999; 9905-0139460.
PR 18-JUN-1999; 9905-0139461.
PR 18-JUN-1999; 9905-0139462.
PR 18-JUN-1999; 9905-0139463.
PR 18-JUN-1999; 9905-0139750.
PR 18-JUN-1999; 9905-0139763.
PR 21-JUN-1999; 9905-0139899.
PR 22-JUN-1999; 9905-0140353.
PR 23-JUN-1999; 9905-0140354.
PR 24-JUN-1999; 9905-0140685.
PR 28-JUN-1999; 9905-0140823.
PR 29-JUN-1999; 9905-0140991.
PR 30-JUN-1999; 9905-0141287.
PR 01-JUL-1999; 9905-0141842.
PR 01-JUL-1999; 9905-0142154.
PR 02-JUL-1999; 9905-0142055.
PR 06-JUL-1999; 9905-0142390.
PR 08-JUL-1999; 9905-0142803.
PR 09-JUL-1999; 9905-0142920.
PR 12-JUL-1999; 9905-0142977.
PR 13-JUL-1999; 9905-0143542.
PR 14-JUL-1999; 9905-0143624.
PR 15-JUL-1999; 9905-0144005.
PR 16-JUL-1999; 9905-0144086.
PR 19-JUL-1999; 9905-0144335.
PR 19-JUL-1999; 9905-0144331.
PR 19-JUL-1999; 9905-0144332.
PR 19-JUL-1999; 9905-0144333.
PR 19-JUL-1999; 9905-0144334.
PR 20-JUL-1999; 9905-0144335.
PR 20-JUL-1999; 9905-0144632.
PR 20-JUL-1999; 9905-0144884.
PR 21-JUL-1999; 9905-0144814.
PR 21-JUL-1999; 9905-0145086.
PR 21-JUL-1999; 9905-0145088.
PR 22-JUL-1999; 9905-0145085.
PR 22-JUL-1999; 9905-0145087.
PR 22-JUL-1999; 9905-0145089.
PR 22-JUL-1999; 9905-0145192.
PR 23-JUL-1999; 9905-0145145.
PR 23-JUL-1999; 9905-0145218.
PR 23-JUL-1999; 9905-0145224.
PR 26-JUL-1999; 9905-0145276.
PR 27-JUL-1999; 9905-0145913.
PR 27-JUL-1999; 9905-0145918.
PR 27-JUL-1999; 9905-0145919.
PR 28-JUL-1999; 9905-0145951.
PR 02-AUG-1999; 9905-0146386.
PR 02-AUG-1999; 9905-0146388.
PR 03-AUG-1999; 9905-0146389.
PR 03-AUG-1999; 9905-0147028.
PR 04-AUG-1999; 9905-0147204.
PR 04-AUG-1999; 9905-0147302.
PR 05-AUG-1999; 9905-0147192.
PR 05-AUG-1999; 9905-0147260.
PR 06-AUG-1999; 9905-0147303.
PR 06-AUG-1999; 9905-0147416.
PR 09-AUG-1999; 9905-0147493.
PR 09-AUG-1999; 9905-0147935.
PR 10-AUG-1999; 9905-0148171.
PR 11-AUG-1999; 9905-0148319.
PR 12-AUG-1999; 9905-0148341.
PR 13-AUG-1999; 9905-0148565.
PR 13-AUG-1999; 9905-0148684.

PR 16-AUG-1999; 9905-0149368.
PR 17-AUG-1999; 9905-0149175.
PR 18-AUG-1999; 9905-0149426.
PR 20-AUG-1999; 9905-0149722.
PR 20-AUG-1999; 9905-0149723.
PR 20-AUG-1999; 9905-0149929.
PR 23-AUG-1999; 9905-0149902.
PR 23-AUG-1999; 9905-0149930.
PR 25-AUG-1999; 9905-0150566.
PR 26-AUG-1999; 9905-0150884.
PR 27-AUG-1999; 9905-0151065.
PR 27-AUG-1999; 9905-0151066.
PR 27-AUG-1999; 9905-0151080.
PR 30-AUG-1999; 9905-0151303.
PR 31-AUG-1999; 9905-0151438.
PR 01-SEP-1999; 9905-0151920.
PR 07-SEP-1999; 9905-0152363.
PR 10-SEP-1999; 9905-0153070.
PR 13-SEP-1999; 9905-0153758.
PR 15-SEP-1999; 9905-0154018.
PR 16-SEP-1999; 9905-0154039.
PR 20-SEP-1999; 9905-0154779.
PR 22-SEP-1999; 9905-0155139.
PR 23-SEP-1999; 9905-0155486.
PR 24-SEP-1999; 9905-0155659.
PR 28-SEP-1999; 9905-0156456.
PR 29-SEP-1999; 9905-0156596.
PR 04-OCT-1999; 9905-0157117.
PR 05-OCT-1999; 9905-0157753.
PR 06-OCT-1999; 9905-0157865.
PR 07-OCT-1999; 9905-0158029.
PR 08-OCT-1999; 9905-0158232.
PR 12-OCT-1999; 9905-0158369.
PR 13-OCT-1999; 9905-0159283.
PR 13-OCT-1999; 9905-0159284.
PR 13-OCT-1999; 9905-0159295.
PR 14-OCT-1999; 9905-0159329.
PR 14-OCT-1999; 9905-0159330.
PR 14-OCT-1999; 9905-0159331.
PR 14-OCT-1999; 9905-0159637.
PR 14-OCT-1999; 9905-0159638.
PR 18-OCT-1999; 9905-0159584.
PR 21-OCT-1999; 9905-0160741.
PR 21-OCT-1999; 9905-0160767.
PR 21-OCT-1999; 9905-0160768.
PR 21-OCT-1999; 9905-0160770.
PR 21-OCT-1999; 9905-0160814.
PR 21-OCT-1999; 9905-0160815.
PR 22-OCT-1999; 9905-0160980.
PR 22-OCT-1999; 9905-0160981.
PR 22-OCT-1999; 9905-0160989.
PR 25-OCT-1999; 9905-0161404.
PR 25-OCT-1999; 9905-0161405.
PR 25-OCT-1999; 9905-0161406.
PR 26-OCT-1999; 9905-0161359.
PR 26-OCT-1999; 9905-0161360.
PR 26-OCT-1999; 9905-0161361.
PR 28-OCT-1999; 9905-0161920.
PR 28-OCT-1999; 9905-0161982.
PR 28-OCT-1999; 9905-0161993.
PR 29-OCT-1999; 9905-0162142.

Query Match 2.3%; Score 50; DB 21; Length 1461.
Best Local Similarity 55.1%; Pred. No. 0.0072;
Matches 98; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
Oy 981 GAACGTCATGAGAGTGAAGTGAAGCCCTGAGACCTACAAATTTAGCTTAC 1040
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 877 GAAGCAAAATGTGAGATCAGATCCCTCCAGCTGCGTATGTACACATCAAAATTCGTCCTTGC 936
Oy 1041 GTTGAATTCGATGAGAGAGATTTATGTATCTGAGAAATTTCTTCATCCCTTGTTCG 1100
    | |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 937 AATCGAAACACAGCTGTTGAGTCATAGCTGACGAGAAAGCTTTCTATGCGCTGCACTC 996

```

Mon Apr 28 09:35:59 2003

us-09-913-858a-1.rng

Page 14

Qy 1101 TGGAACTGTCCCTGTGGTGTGGTGCCTCAATATATCAGGACTTTCCTTCCT 1158
||| ||| | | | | | | | | | | | | | | | |
Db 997 TGGTCTGTTCCAATCTATTTTGGGGCCCTTAACGTGCAAGACTTGTGCCCTCGCAT 1054

Search completed: April 28, 2003, 01:22:46
Job time : 502 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 01:10:31 ; Search time 2820 Seconds
(Without alignments)
12623.291 Million cell updates/sec

Title: US-09-913-858a-1
Perfect score: 2198
Sequence: 1 actaactcaacgctgcatc.....aaaaaaaaaaaaaaaaaaaaa 2198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estbda:*
2: em_estbhm:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	437.6	19.9	532	13	BM143091 saj39d07.
2	378.6	17.2	689	13	BM099511 BBS01_SQ
3	337.2	15.3	571	13	BJ464838 BJ464838
4	332.2	15.1	517	12	BG790911 BG790911
5	280.2	12.7	690	14	BQ659171 BQ659171
6	257.8	11.7	701	14	BQ167130 BQ167130

7	248.8	11.3	856	10	BE412601
8	231.2 <td>10.5 <td>803 <td>12 <td>BF626851</td> </td></td></td>	10.5 <td>803 <td>12 <td>BF626851</td> </td></td>	803 <td>12 <td>BF626851</td> </td>	12 <td>BF626851</td>	BF626851
9	223.8 <td>10.2 <td>420 <td>9 <td>AJ475410</td> </td></td></td>	10.2 <td>420 <td>9 <td>AJ475410</td> </td></td>	420 <td>9 <td>AJ475410</td> </td>	9 <td>AJ475410</td>	AJ475410
10	218.8 <td>10.0 <td>700 <td>9 <td>AL503218</td> </td></td></td>	10.0 <td>700 <td>9 <td>AL503218</td> </td></td>	700 <td>9 <td>AL503218</td> </td>	9 <td>AL503218</td>	AL503218
11	212.6 <td>9.7 <td>729 <td>14 <td>BM816799</td> </td></td></td>	9.7 <td>729 <td>14 <td>BM816799</td> </td></td>	729 <td>14 <td>BM816799</td> </td>	14 <td>BM816799</td>	BM816799
12	208	9.5 <td>560 <td>14 <td>BM737488</td> </td></td>	560 <td>14 <td>BM737488</td> </td>	14 <td>BM737488</td>	BM737488
13	195.2	8.9 <td>12 <td>12 <td>BG465531</td> </td></td>	12 <td>12 <td>BG465531</td> </td>	12 <td>BG465531</td>	BG465531
14	191	8.7 <td>383 <td>13 <td>BM443222</td> </td></td>	383 <td>13 <td>BM443222</td> </td>	13 <td>BM443222</td>	BM443222
15	189	8.6 <td>321 <td>12 <td>BG263065</td> </td></td>	321 <td>12 <td>BG263065</td> </td>	12 <td>BG263065</td>	BG263065
16	187.2	8.5 <td>674 <td>13 <td>BJ170811</td> </td></td>	674 <td>13 <td>BJ170811</td> </td>	13 <td>BJ170811</td>	BJ170811
17	179	8.1 <td>844 <td>12 <td>BF261629</td> </td></td>	844 <td>12 <td>BF261629</td> </td>	12 <td>BF261629</td>	BF261629
18	172.8	7.9 <td>388 <td>14 <td>BQ462317</td> </td></td>	388 <td>14 <td>BQ462317</td> </td>	14 <td>BQ462317</td>	BQ462317
19	156.4	7.1 <td>666 <td>17 <td>BH431446</td> </td></td>	666 <td>17 <td>BH431446</td> </td>	17 <td>BH431446</td>	BH431446
20	156.4	7.1 <td>753 <td>17 <td>BH418424</td> </td></td>	753 <td>17 <td>BH418424</td> </td>	17 <td>BH418424</td>	BH418424
21	151.8	6.9 <td>735 <td>17 <td>BH423619</td> </td></td>	735 <td>17 <td>BH423619</td> </td>	17 <td>BH423619</td>	BH423619
22	146	6.6	526	9 <td>AL500587</td>	AL500587
23	141.8	6.5	669 <td>17 <td>BH7847</td> </td>	17 <td>BH7847</td>	BH7847
24	136.8	6.2	772 <td>17 <td>BH535486</td> </td>	17 <td>BH535486</td>	BH535486
25	134.4	6.1	806 <td>17 <td>BH441710</td> </td>	17 <td>BH441710</td>	BH441710
26	133.8	6.1	269 <td>10 <td>AM695306</td> </td>	10 <td>AM695306</td>	AM695306
27	133.6	6.1	543 <td>17 <td>CNS00M0V</td> </td>	17 <td>CNS00M0V</td>	CNS00M0V
28	131.6	6.0	484 <td>14 <td>BM737489</td> </td>	14 <td>BM737489</td>	BM737489
29	130	5.9	496 <td>10 <td>AM498425</td> </td>	10 <td>AM498425</td>	AM498425
30	127.4	5.8	539 <td>17 <td>BH783802</td> </td>	17 <td>BH783802</td>	BH783802
31	111	5.1	529 <td>14 <td>BQ765453</td> </td>	14 <td>BQ765453</td>	BQ765453
32	110	5.0	240	9 <td>AJ477062</td>	AJ477062
33	105	4.8	604 <td>17 <td>AQ271924</td> </td>	17 <td>AQ271924</td>	AQ271924
34	105	4.8	616 <td>17 <td>AQ328306</td> </td>	17 <td>AQ328306</td>	AQ328306
35	104.6	4.8	344 <td>17 <td>BH440694</td> </td>	17 <td>BH440694</td>	BH440694
36	101.6	4.6	791 <td>10 <td>BE034958</td> </td>	10 <td>BE034958</td>	BE034958
37	101	4.6	472 <td>12 <td>BG241740</td> </td>	12 <td>BG241740</td>	BG241740
38	96.4	4.4	500 <td>14 <td>BM885010</td> </td>	14 <td>BM885010</td>	BM885010
39	89.8	4.1	568 <td>13 <td>BJ201098</td> </td>	13 <td>BJ201098</td>	BJ201098
40	86.2	3.9	235 <td>14 <td>BQ629003</td> </td>	14 <td>BQ629003</td>	BQ629003
41	84.6	3.8	433 <td>10 <td>AV792413</td> </td>	10 <td>AV792413</td>	AV792413
42	84.4	3.8	501 <td>13 <td>BI922470</td> </td>	13 <td>BI922470</td>	BI922470
43	78.6	3.6	663 <td>17 <td>AQ158899</td> </td>	17 <td>AQ158899</td>	AQ158899
44	78.6	3.6	772 <td>17 <td>AQ840447</td> </td>	17 <td>AQ840447</td>	AQ840447
45	73.8	3.4	566 <td>17 <td>BH776651</td> </td>	17 <td>BH776651</td>	BH776651

ALIGNMENTS

RESULT 1
LOCUS BM143091 532 bp mRNA linear EST 29-NOV-2001
DEFINITION saj39d07.y1 Gm-c1066 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1066-5150 5' similar to TR:Q9ST51 Q9ST51 FUCT C3 PROTEIN. ; mRNA sequence.

ACCESSION BM143091.1 GI:17153158
VERSION
KEYWORDS
SOURCE
ORGANISM

soybean.
Glycine max

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosids I: Fabales: Fabaceae: Papilionoideae: Phaseoleae: Glycine.

REFERENCE
AUTHORS

1 (bases 1 to 532)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corvelli, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, T., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schenk, R., Ritter, E., Kohn, S., Shio, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

TITLE
JOURNAL
COMMENT

QY 1117 GTGTGTCGCTCCAAATATTCAGAGCTTTCCTCTCTCCGTGTCATTTTACATATT 1176
 11 111111 11 111111 11 1111 11 11111111 11
 Db 241 GTCCTTGCCGACCGAATATTCAGAGCTTTCCTCCAGAGAGATGCAATATTCACATC 300
 11 111111 11 111111 11 111111 11 111111 11
 QY 1177 AAGAGATAGAGATGTTGAGCTGTGTGCAAGACCATGAGATATTCAGCAAAATCCC 1236
 11 1111 11 111111 11 111111 111111 111111 111111
 Db 301 AAGAGCTTATGATGATTCATTTTCAGTTGCGAAGCAATGAAACATATTCGTCAAATCCT 360
 11 1111 11 111111 11 111111 111111 111111 111111
 QY 1237 GAAGCATATATCATCATTCATTCAGAGTATGAGGATGAGGATTCAGTCTTCCTTAAGGCC 1296
 11 111111 11 111111 111111 111111 111111 111111 111111
 Db 361 GATGCTTTTATCATCATTCATTCAGAGTATGAGGATGAGGATTCAGTCTTCCTTAAGGCC 420
 11 111111 11 111111 111111 111111 111111 111111 111111
 QY 1297 CTGTGATATGCGAGCTGTGCATTCATCGTCCGCTTTGTCATTCAGTTCGCAAGATG 1356
 11 111111 11 111111 111111 111111 111111 111111 111111
 Db 421 CTATATGACATGCGAGGCTTTCATTCATTCGCTTCCTTTATATCATATGCTTACAGCA 480
 11 111111 11 111111 111111 111111 111111 111111 111111
 QY 1357 AGTGAAG 1416
 11 111111 11 111111 111111 111111 111111 111111 111111
 Db 481 ATTCAT 540
 11 111111 11 111111 111111 111111 111111 111111 111111
 QY 1417 GGGCCAAACCGTAT 1476
 11 111111 11 111111 111111 111111 111111 111111 111111
 Db 541 AAAAG 600
 11 111111 11 111111 111111 111111 111111 111111 111111
 QY 1477 ATTACCTGAGCTTACCAATTTTACTCTGATCTGTAAGGCTGCTGTTGTTTGAAG 1536
 11 111111 11 111111 111111 111111 111111 111111 111111
 Db 601 ATTATCTAGATCATGATCATGATTTTAACTTTAGAGCTTTGAAGTGTGCTGTCAGATATA 660
 11 111111 11 111111 111111 111111 111111 111111 111111
 QY 1537 TTGACATCCCTGAATCTTGTGCTGTATG 1565
 11 111111 11 111111 111111 111111 111111 111111 111111
 Db 661 TTTAGCTCCCTCAAGCATGTTCTATATG 689
 11 111111 11 111111 111111 111111 111111 111111 111111

RESULT 3

BJA64838 571 bp mRNA linear EST 23-MAY-2002
 LOCUS BJA64838 K. Sato unpublished cDNA library, cv. Haruna Nijo
 DEFINITION germination shoots Hordeum vulgare subsp. vulgare cDNA clone
 bags36d24 5', mRNA sequence.

ACCESSION BJA64838
 VERSION BJA64838.1 GI:21143345

SOURCE Hordeum vulgare subsp. vulgare.
 ORGANISM Hordeum vulgare subsp. vulgare.

REFERENCE 1 (bases 1 to 571)
 AUTHORS Sato, K., Saisho, D. and Takeda, K.
 TITLE Barley EST sequencing project in NIG and Okayama Univ
 JOURNAL Unpublished (2002)
 COMMENT Contact: Tadasi Shii-1
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshii@genes.nig.ac.jp.

FEATURES

Source

1. 571
 /organism="Hordeum vulgare subsp. vulgare"
 /cultivar="Haruna Nijo"
 /db_xref="taxon:112509"
 /clone="bags36d24"
 /clone_1lb="K. Sato unpublished cDNA library, cv. Haruna
 Nijo germination shoots"
 /tissue_type="shoots"
 /dev_stage="germination"
 BASE COUNT 164 a 109 c 131 g 167 t

Query Match 15.3%; Score 337.2; DB 13; Length 571;
 Best Local Similarity 75.4%; Pred. No. 1.3e-50;

Matches 433; Conservative 0; Mismatches 138; Indels 3; Gaps 1;
 QY 718 GAATATATATGCTGGAACAAATATATGCTTGGCAAGAGAGAGATATATATATG 777
 11 111111 11 111111 11 1111 11 111111 11
 Db 1 GAATATATATGCTGGAACAAATATATGCTTGGCAAGAGAGATATATATATG 57
 11 111111 11 111111 11 1111 11 111111 11
 QY 778 ACAACCACTATATGCTGGAATGCTTCCGTTGATATATATATGAGTATGATG 837
 11 111111 11 111111 11 1111 11 111111 11
 Db 58 ACAACCACTATATGCTGGAATGCTTCCGTTGATATATATGAGTATGATG 117
 11 111111 11 111111 11 1111 11 111111 11
 QY 838 ATGGACCACTGACAGCCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 897
 11 111111 11 111111 11 1111 11 111111 11
 Db 118 ATGGACCACTGACAGCCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 177
 11 111111 11 111111 11 1111 11 111111 11
 QY 898 GGTGCTGAATTTTCCGTTGCAAGCTTGTGAGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 957
 11 111111 11 111111 11 1111 11 111111 11
 Db 178 GGTGCTGAATTTTCCGTTGCAAGCTTGTGAGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 237
 11 111111 11 111111 11 1111 11 111111 11
 QY 958 GATTCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1017
 11 111111 11 111111 11 1111 11 111111 11
 Db 238 GATTCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 297
 11 111111 11 111111 11 1111 11 111111 11
 QY 1018 AAGCACTACAAATTTAGCTTACGTTGAAATTCGAAATGAGAGAGATATATATGAGAA 1077
 11 111111 11 111111 11 1111 11 111111 11
 Db 298 AAGGCTACAAATTTAGCTTACGTTGAAATTCGAAATGAGAGAGATATATATGAGAA 357
 11 111111 11 111111 11 1111 11 111111 11
 QY 1078 AATTTCTTCCATCCCTTGTGCTGGAAGTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1137
 11 111111 11 111111 11 1111 11 111111 11
 Db 358 AAGTCTTTCAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 417
 11 111111 11 111111 11 1111 11 111111 11
 QY 1138 CAGGACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1197
 11 111111 11 111111 11 1111 11 111111 11
 Db 418 CAGGACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 477
 11 111111 11 111111 11 1111 11 111111 11
 QY 1198 TCTGTGCAAG 1257
 11 111111 11 111111 11 1111 11 111111 11
 Db 478 TCAGTGTGCAAG 537
 11 111111 11 111111 11 1111 11 111111 11
 QY 1258 AGGTGGAAGTATGAG 1291
 11 111111 11 111111 11 1111 11 111111 11
 Db 538 AGGTGGAAGTATGAG 571
 11 111111 11 111111 11 1111 11 111111 11

RESULT 4

BG790911

LOCUS BG790911 517 bp mRNA linear EST 29-NOV-2001
 DEFINITION sae71e02.y1 Gm-cl064 Glycine max cDNA clone GENOME SYSTEMS CLONE
 ID: Gm-cl064-3675 5' similar to TR:Q95751 Q95751 FUCT C3 PROTEIN.
 ;, mRNA sequence.

ACCESSION BG790911
 VERSION BG790911.1 GI:14126473

KEYWORDS EST.
 SOURCE soybean.

REFERENCE 1 (bases 1 to 517)
 AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelidg, J., Coryell, V., Khanna
 A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers
 Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schuck
 R., Riller, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
 R., Waterston, R. and Wilson, R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Shoemaker R/Public Soybean EST project
 Public Soybean EST project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

DB 450 CCAGCAAAAGAGACAGATACACTATTTCAGAGAGAGAGCGGCTTAAGACAG 391
 QY 1472 AGCCATTACCGAGAGTACAGATTTACCTGATGCTGGAAGCGCTGCTTT 1531
 DB 390 AGACATTTTATCTAATACATGATCAGTACCTTAGAGCTTTGAGCTGTCAGC 331
 QY 1532 TGAAGTTCATCCCTGATCTGCTGCTGATGAGAGACTGAAGCGCTGAATTATA 1591
 DB 330 ATTAATTTAGCTCCCAAGCATGCTTCATATGAGAAAGATGAAGGCCATCAAGTTC 271
 QY 1592 GAGGGGAGAGCTTTAAACTCTACAAAATATACCAATTTGCTGACAGACAG 1651
 DB 270 GAGGTGGGATGAAATGAAGGTGACAAAATTTATCCAAATAGGCTTACAGACAGCAAG 211
 QY 1652 CTCTTATACCTTCACCTTCACAAAGTGATGCTATTTACAGAGTCTGAGAACATC 1711
 DB 210 CGTTATATTAATTTCAATTCATGAGAGATGCTAAGTCTAGATATATTAAGGCGCATC 151
 QY 1712 CTGTGCAAGTTTGAAGTCAATTTTGTGAC 1744
 DB 150 CATGTGCAAGCTTGAAGTCAATTTTGTATAC 118

RESULT 6
 LOCUS BQ167130/c 701 bp mRNA linear EST 25-APR-2002
 DEFINITION WHE0946_F09_K182Y wheat 5-15 DAP spike cDNA library Triticum
 aestivum cDNA clone WHE0946_F09_K18, mRNA sequence.
 ACCESSION BQ167130
 VERSION BQ167130.1 GI:20311201
 KEYWORDS EST.
 SOURCE bread wheat.
 ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 Triticeae; Triticum.
 1 (bases 1 to 701)
 Anderson, O.D., Cho, S., Choi, D.W., Close, T.J., Fenton, R.D., Han,
 P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
 Seaton, C.L. and Tong, J.C.

The structure and function of the expressed portion of the wheat
 genomes - 5-15 DAP spike cDNA library
 Unpublished (2000)
 Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818

Email: oanderson@w.usda.gov
 This EST was generated by sequencing from the 3' end of the clone.
 Sequences have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20.
 Seq primer: Oligo dt wobble primer (an equal mixture of (T)27A, (T
)27G and (T)27C).

FEATURES
 source location/Qualifiers

1..701
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE0946_F09_K18"
 /clone_lib="Wheat 5-15 DAP spike cDNA library"
 /tissue_type="spike"
 /dev_stage="Adult Plant"
 /lab_host="E. coli SOLR"
 /note="Vector: Lambda uni-ZAP XR, excised phagemid;
 site_1: EcoRI; site_2: XhoI; Plants were grown in the
 greenhouse. Spikes at 5, 10 and 15 DAP were harvested,
 total RNA and poly(A) RNA were prepared, a cDNA library
 was made, and the cDNA clones were in vivo excised to
 give Bluescript phagemids in the TJ Close lab (Choi,
 Close, Fenton) at the University of California,

Riverside. Plasmid DNA preparations and DNA sequencing
 were performed in the OD Anderson lab (all other authors
)

BASE COUNT 218 a 153 c 124 g 206 t
 ORIGIN
 Query Match 11.7%; Score 257.8; DB 14; Length 701;
 Best Local Similarity 68.2%; Pred. No. 1.7e-36;
 Matches 358; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

QY 1220 ATCTAGCAGAAATCCCGAAGCATATATATCATCATTTGAGGTGAGATGAGGCTCAT 1279
 DB 701 ATATTGATCGAATCTGATGCTTTTATCAATCTTGAAGTGAATGATGATGCTCAT 642
 QY 1280 CTGACCTCCCAAGCGCCCTGATATGACGTGACGTGCACTTCACTGCGCTTTGCA 1339
 DB 641 CTGATCTTTTCAAGCAGCTTATGATGACATGACGAGGCTTCACTGCGCTTTGCA 582
 QY 1340 TTCACTTGCCACAGTGTAGTAGAGAGAGAGAAATATATCCAGCCTTAAGAGAGCTC 1399
 DB 581 TACATATCGCTACGAGAGATTCACGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 522
 QY 1400 CTTCAGAGTCACTAGAGAGGCGCAGAAACCTATATCATATCTATGTCAGAGAGAGGAA 1459
 DB 521 CATGTAGCTTCTCCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 462
 QY 1460 GGTTCGATGAGAGTCACTTACCTGAGTCTGACATTTTACCTGCAATGCTGTGAGG 1519
 DB 461 GGTTCGATGAG 402
 QY 1520 CTGCTGTTGTTTGAAGTTCACATCTTGAATCTTGTGCTGATGAGAGAGAGAGAG 1579
 DB 401 CTGCGCTGATGAGTAAATTTAGATCCCTCAAGAGATGCTGATAGAGAGAGAGAGAG 342
 QY 1580 CTGAGTTATAG 1639
 DB 341 CATCAAGTATTCGAG 282
 QY 1640 CACAGAGACAGAGCTTATACCTGATGAGTCAAGGTGAGTGGATTCAGAGAGAGTACT 1699
 DB 281 CAGAGAGACAGAGCTTATATTAATTTCAATTCAGTGAATGAGAGAGAGAGAGAG 222
 QY 1700 TGGAGACAATCCCTTGTGCCAGATTGAGTCAATTTTGTGTAGC 1744
 DB 221 TTAAGGGCATTCATGTGCAAGGTGAGTGAATTTTGTATATAC 177

RESULT 7
 LOCUS BE412601 856 bp mRNA linear EST 24-JUL-2000
 DEFINITION MCG002_B07R990625 ITTC MCG Barley Leaf/Culm Library Hordeum vulgare
 BE412601
 VERSION BE412601.1 GI:9410447
 KEYWORDS EST.
 SOURCE Hordeum vulgare.
 ORGANISM Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 Triticeae; Hordeum.
 1 (bases 1 to 856)

REFERENCE
 AUTHORS Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier,
 S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,
 Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P.,
 Langridge, P., Lazo, G.R., Lin, J.J., McQuill, P., Ogihara, Y.,
 Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M.,
 Sorrells, M., Warburton, M. and Wenzel, G.
 International Triticale EST Cooperative (ITTC): Production of
 Expressed Sequence Tags for Species of the Triticeae
 Unpublished (2000)
 CONTACT: Graner A
 Institute for Plant Genetics & Crop Plant Research
 Corrensstr. 3, D-06466 Gatersleben GERMANY


```

FEATURES
    source
        location/Qualifiers
            1..560
                /organism="Zea mays"
                /cultivar="BMS (Black Mexican Sweet)"
                /db_xref="taxon:4577"
                /clone_lib="952 - BMS tissue from Walbot Lab (reduced RNA
                )"
                /tissue_type="suspension culture"
                /dev_stage="mixed logarithmic and stationary growth
                phases"
                /lab_host="DH10B"
                /note="Vector: pUC19, Site_1: EcoRI, Site_2: EcoRI. The
                library was prepared by George Rudenko using poly (A)
                selected RNA and Universal Riboclone cDNA Synthesis System

```

RESULT 13					
LOCUS	BG465531				
DEFINITION	619 bp	mRNA	linear	EST 20-MAR-2001	
	RG465531				
	RH122_05.F10.b1_A003	Rhizome2 (RH122)	Sorghum propinquum	cdNA, mRNA	
	sequence.				
ACCESSION	RG465531				
VERSION	RG465531.1				
KEYWORDS	GI:13394507				
SOURCE	EST.				
ORGANISM	Sorghum propinquum.				
	Sorghum propinquum				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC				
	clade; Panicoideae; Andropogoneae; Sorghum.				
REFERENCE	1 (bases 1 to 619)				
AUTHORS	Cordonnier-Pratt,M.-M., Gingle,A., Paterson,A., Sudman,M. and Pratt				
	,L.H.				
TITLE	An EST database from Sorghum: Sorghum propinquum rhizomes				
JOURNAL	unpublished (2000)				

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 01:12:16 ; Search time 117 Seconds
(without alignments)
5761.329 Million cell updates/sec

Title: US-09-913-858a-1

Perfect score: 2198
Sequence: 1 actaactcaaacgctgcatt.....aaaaaaaaaaaaaaaaaaaaa 2198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/prodata1/lna/5A_COMB.seq:*
2: /cgn2_6/prodata1/lna/5B_COMB.seq:*
3: /cgn2_6/prodata1/lna/6A_COMB.seq:*
4: /cgn2_6/prodata1/lna/6B_COMB.seq:*
5: /cgn2_6/prodata1/lna/PCTUS_COMB.seq:*
6: /cgn2_6/prodata1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209.4	9.5	2069	4	US-09-678-300-3
2	209.4	9.5	2124	4	US-09-678-300-6
3	209.4	9.5	2165	4	US-09-678-300-9
4	209.4	9.5	2232	4	US-09-678-300-12
5	209.4	9.5	2808	4	US-09-678-300-2
6	209.4	9.5	2863	4	US-09-678-300-5
7	209.4	9.5	2904	4	US-09-678-300-8
8	209.4	9.5	2971	4	US-09-678-300-11
9	209.4	9.5	3714	4	US-09-678-300-1
10	44.4	2.0	1639	2	US-08-737-524B-1
11	42.4	1.9	665	4	US-08-998-416-185
12	42.4	1.9	662	4	US-08-998-416-137
13	42.4	1.9	701	4	US-08-998-416-701
14	42.4	1.9	711	4	US-08-998-416-786
15	42.4	1.9	724	4	US-08-998-416-683
16	42.4	1.9	732	4	US-08-998-416-1036
17	42.4	1.9	828	4	US-08-998-416-538
18	42.4	1.9	834	4	US-08-998-416-305
19	42.4	1.9	863	4	US-08-998-416-191
20	42.4	1.9	860	4	US-08-998-416-287
21	40.6	1.8	7218	1	US-08-232-463-14
22	40.4	1.8	854	4	US-08-998-416-534
23	39.4	1.8	3573	4	US-09-353-585-1
24	38.6	1.8	6124	4	US-08-213-4198-3
25	38.2	1.7	7218	1	US-08-232-463-14
26	38.2	1.7	1454	1	US-08-220-958-3
27	37.8	1.7	723	2	US-08-618-911-1

28	37.8	1.7	767	4	US-08-998-416-472	Sequence 472, App
29	37.8	1.7	837	4	US-08-998-416-535	Sequence 535, App
30	37.8	1.7	1578	4	US-09-416-050A-1	Sequence 1, Appl
31	37.8	1.7	1578	4	US-09-664-800-1	Sequence 1, Appl
32	37.8	1.7	1578	4	US-09-665-309-1	Sequence 1, Appl
33	37.8	1.7	1578	4	US-09-661-569-1	Sequence 1, Appl
34	37.8	1.7	4673	1	US-07-638-431-1	Sequence 1, Appl
35	37.8	1.7	4673	5	PCT-US92-00018-1	Sequence 1, Appl
36	37.6	1.7	1371	2	US-08-428-713-1	Sequence 1, Appl
37	37.6	1.7	1371	3	US-08-904-179-1	Sequence 1, Appl
38	37.4	1.7	87350	3	US-08-781-891-79	Sequence 79, Appl
39	37.4	1.7	87343	4	US-09-791-211-3	Sequence 389, App
40	37.2	1.7	629	4	US-09-385-982-389	Sequence 11, Appl
41	36.8	1.7	1058	4	US-09-452-239-11	Sequence 1, Appl
42	36.8	1.7	1353	4	US-09-173-300-3	Sequence 3, Appl
43	36.2	1.6	2073	4	US-09-819-993-1	Sequence 1, Appl
44	36.2	1.6	2002	4	US-09-116-498-1	Sequence 1, Appl
45	35.8	1.6	1026	4	US-09-116-498-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-678-300-3
Sequence 3, Application US/09678300
Patent No. 6420548
GENERAL INFORMATION:
APPLICANT: VOZINA, Louis-Philippe
APPLICANT: D'Aoust, Marc-Andr
TITLE OF INVENTION: MEDICAGO INC.
TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
FILE REFERENCE: 14149-3"PCT"
CURRENT APPLICATION NUMBER: US/09/678, 300
CURRENT FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US 60/157,133
PRIOR FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2069
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequences to be used as promoter for regulating
OTHER INFORMATION: expression of foreign genes
US-09-678-300-3

Query Match 9.5%; Score 209.4; DB 4; Length 2069;
Best Local Similarity 66.5%; Pred. No. 2.9e-51;
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

QY	1486	AGGCTGACCAATTTACTGTAATGCTGTGAAGCGCTGTTGTTGAAGTTCATC	1545
DB	170	AGAGTACCAATTTACTGTAATGCTGTGAAGCGCTGTTGTTGAAGTTCATC	229
QY	1546	CTGATCTTGCGCTGTAATGTAAGCAAGCTGTAAGTTCATC	1605
DB	230	CTGATCTTGCGCTGTAATGTAAGCAAGCTGTAAGTTCATC	289
QY	1606	TTAAACCTGCAAAATTTATCCCAATGGCTTGAACAGACAGCAAGCTTATACCTTC	1665
DB	290	TTGAAGGTTTCAAAATTTATCCCTGCGGCTTGACACAGAGCAAGCTTATACCTTC	349
QY	1666	AGCTTCAAGGTAATGCTGATTCAGAGTCACTTGGAAGCAATCTTGTGCCAAGTTT	1725
DB	350	CAGTTCAAGGTAATGCTGATTCAGAGTCACTTGGAAGCAATCTTGTGCCAAGTTT	409
QY	1726	GAACTCATTTTGTGTCAGATGCGCTAA-----ATGCTACCTCTGCTACCTGATTT	1778
DB	410	GAACTCATTTTGTGTCAGATGCGCTAA-----ATGCTACCTCTGCTACCTGATTT	469

OY	1779	AGCTTCACTTACGCTGACCACTACTACTGAGTTTGGAAAGACATATGGCAAGTCAATATGGC	1838
Db	470	AGCTCTTTCACTTACTACTGAGACAGATCAAGTTTGGAAATGAGTATGACCATGGAATCGGC	529
OY	1839	ATGGCTT-----TATTATATGCGTATGTTCTTGGCCAACTCATATGATGTTT	1884
Db	530	ATGGCTTTGTAATCCCTACCCCTACTTTGGCCAACTCATGCGGGATTTACATTCACAAAT	589
OY	1885	GTAATAGACATCACACTTTTAATTTTAACTGTTTCTGTAGAACGTGCAATCCATATTTA	1944
Db	590	ATATACATCACTTCAACCCCTACTTAAACCCCTTTTGTATGATTAACGAATGTTCAATATTTA	649
OY	1945	ATGCTAGTTTATGTCCTTATCTATGATCAT	1977
Db	650	ATGTTGGCTTGTAAGTCTTTTACTTGATTAAT	682

```

RESULT 2
US-09-678-300-6
Sequence 6, Application US/09678300
Patent No. 6420548
GENERAL INFORMATION:
APPLICANT: VOZINA, Louis-Philippe
APPLICANT: D'Aoust, Marc-Andr  
APPLICANT: MEDICAGO INC.
TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
FILE REFERENCE: 14149-3"PCT"
CURRENT APPLICATION NUMBER: US/09/678,300
CURRENT FILING DATE: 2000-10-03
PRIORITY FILING DATE: 1999-10-04
PRIORITY FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 2124
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequences to be used as promoter for regulating
US-09-678-300-6
OTHER INFORMATION: expression of foreign genes

```

```

Db      530  ATGGCTTTGTAATGCCCAACCTACTTTGGCCAACTCATGGGGATTTCATTACATTGAGAAAT 589
Oy      1885  GTATAGACATGCACACTTTAAATTTTAAACCTGTTCTGTAGAAAGTCACAAATCCATATTTTA 1944
Db      590  ATACATGCTTCTCAACCACTACTTAAACCCCTTTTGTATGATTAACGTAAATGATGTTCAATTTTA 649
Oy      1945  ATGCTTACTTTTAGTGCTCTATATGATCAATCT 1977
Db      650  ATGTTGGTTGTAGTGTTTACTTACTGATTAAT 682

RESULT 3
US-09-678-300-9
; Sequence 9, Application US/09678300
; Patent No. 6420548
; GENERAL INFORMATION:
; APPLICANT: VOZINA, Louis-Philippe
; APPLICANT: D'AUOST, Marc-Andr 
; APPLICANT: MEDICAGO, INC.
; TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
; TITLE OF INVENTION: FOREIGN GENES
; FILE REFERENCE: 14149-3-Pct 
; CURRENT APPLICATION NUMBER: US/09/678,300
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/157,133
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Sequences to be used as promoter for regulating
; OTHER INFORMATION: expression of foreign genes
US-09-678-300-9

```


CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38, 241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 937:
SEQUENCE CHARACTERISTICS:
LENGTH: 665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1581RP
US-08-998-416-937

Query Match 1.9%; Score 42.4; DB 4; Length 665;
Best Local Similarity 46.9%; Pred. No. 0.013;
Matches 165; Conservative 0; Mismatches 186; Indels 1; Gaps 1;

1845 TTATTATGCTAGTCTTGGCCACACTGATGTTTGTATAGACATCACACTTTA 1904
196 TTGATTTATTTATCTATTTAACAATAAATTTTAAATGTTTAAATAAATAAATA 255
1905 ATTTTAACTGTTTCTGTAGAAATGCAATCCATATTTTATGCTTTAGTCTCT 1964
256 CTATAGAAATTTATTAATAATAGATTTAATTTAATTTAAT -ATTAAATATACATTTT 314
1965 TATCTGATCATCTAGAGTACAGACTCTTGATATTTGTGAGTGAACCTGAATCTATA 2024
315 TATTAATAAATAGATTTTAAATTTAATAATTAATTAATTAATTTAATTAATA 374
2025 GAAGATCAGATGTTTGCACACACATTTACTTACTGTTTGTGATGATCTCGA 2084
375 AATTAATTTATTTACTTCATTTGATATATTAATTAATTAATTAATTTAATTTA 434
2085 GCTTTTATAGTCTGGAAGTCCCTGCTGTTGAGCAGCTGTTATGCTTCACTGTTA 2144
435 TTTTATTAAGTCTGATTAATTTCTATTTAATAGTCTACCTTTAATTTGATATTTAC 494
2145 CTGCGCAGTGTATGCTTTTGGACCTCTAATAAAAAAAAAAAAAAAAAAAAAA 2196
495 CTACTAATAATTTACCTAATAATTAATTAATTAAGAAATCTTAATCTAATAA 546

RESULT 13
US-08-998-416-701
Sequence 701, Application US/08998416

Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippson, Peter
APPLICANT: Philippson, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Reibschung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38, 241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 701:
SEQUENCE CHARACTERISTICS:
LENGTH: 701 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1462RP
US-08-998-416-701

Query Match 1.9%; Score 42.4; DB 4; Length 701;
Best Local Similarity 46.9%; Pred. No. 0.014;
Matches 165; Conservative 0; Mismatches 186; Indels 1; Gaps 1;

1845 TTATTATGCTAGTCTTGGCCACACTGATGTTTGTATAGACATCACACTTTA 1904
196 TTGATTTATTTATCTATTTAACAATAAATTTTAAATGTTTAAATAAATAAATA 255
1905 ATTTTAACTGTTTCTGTAGAAATGCAATCCATATTTTATGCTTTAGTCTCT 1964
256 CTATAGCAATTTTATTAATAATAGATTTAATTTAATTTAAT -ATTAAATATACATTTT 314
1965 TATCTGATCATCTAGAGTACAGACTCTTGATATTTGTGAGTGAACCTGAATCTATA 2024
315 TATTAATAAATAGATTTTAAATTTAATAATTAATTAATTAATTAATTTAATA 374
2025 GAAGATCAGATGTTTGCACACACATTTACTTACTGTTTGTGATGATCTCGA 2084
375 AATTAATTTATTTACTTCATTTGATATATTAATTAATTAATTTAATTTAATTTA 434
2085 GCTTTTATAGTCTGGAAGTCCCTGCTGTTGAGCAGCTGTTATGCTTCACTGTTA 2144
435 TTTTATTAAGTCTGATTAATTTCTATTTAATAGTCTACCTTTAATTTGATATTTAC 494
2145 CTGCGCAGTGTATGCTTTTGGACCTCTAATAAAAAAAAAAAAAAAAAAAAAA 2196
495 CTACTAATAATTTACCTAATAATTAATTAATTAAGAAATCTTAATCTAATAA 546

RESULT 14
US-08-998-416-786
Sequence 786, Application US/08998416

Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippson, Peter
APPLICANT: Philippson, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Reibschung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF

Mon Apr 28 09:35:59 2003

Search completed: April 28, 2003, 03:45:53
Job time : 157 secs

us-09-913-858a-1.rni

RESULT 2
US-09-878-574-7836
; Sequence 7836, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 7836
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701100402H1
US-09-878-574-7836

Query Match 3.88; Score 83.4; DB 10; Length 273;
Best Local Similarity 79.48; Pred. No. 2.5e-13;
Matches 112; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
QY 984 CCGGATGAGAGTGAACAAGTGAAGCCCTGAGACCTACAAATTTAGCTTACGCTT 1043
DB 1 CCGGATGAGAGTGAACAAGTGAAGCCCTGAGACCTACAAATTTAGCTTACGCTT 60
QY 1044 TGAATATTCGATGAGAGATTTATGTAAGTGAATAAT--TCTTCCATTCCTTGTGTC 1100
DB 61 TGAGAAATTCGATGAGATTTATGTAAGTGAATAATGCTGTGACATGCAATGCTTGTAC 120
QY 1101 TGAACCTGCTCCCTGTGCTGT 1121
DB 121 TGAATCTAAGAGTGTGGTGT 141

RESULT 3
US-09-918-995-2051
; Sequence 2051, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2051
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(477)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2051

Query Match 2.28; Score 49.2; DB 9; Length 477;
Best Local Similarity 49.28; Pred. No. 0.0017;
Matches 129; Conservative 0; Mismatches 133; Indels 0; Gaps 0;
QY 1007 TGAAGCCCTGAACGATTAACATTTAGCTTGAATAATTCGATGAGAGATTT 1066
DB 75 TGGCTTCTCTGTCCCGCTATATAGTTCACCTTGGCCCTGGAATAATGCCATCTGTACGACT 134

QY 1067 ATGTAAGTGAATAATTTCTCCAAATCCCTTGTGCTGGAAGTCTCCCTGTGCTG 1126
DB 135 ACATGACGAGAAAAGCTGTGGCGTCCCATGACACCTGGCGGCTGTGACCGCGTT 194
QY 1127 CTCCTGATATTCAGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1186
DB 195 CTCCTGATGAGGAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 254
QY 1187 AGAATGCTGAGTCTGTCGCAAGACCATATATATATATATATATATATATATATAT 1246
DB 255 AGTCTCTCAGACAGCTGAGAGATTTATTTGACTTTCTGACAGAGAGATGAGATATA 314
QY 1247 ATCAATCATTTGAGGTGGAAGTA 1268
DB 315 TGAATATACCTGCGATATACAGCA 336

RESULT 4
US-09-960-352-12673/C
; Sequence 12673, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.008/37-21(102981C)
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 12673
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 54-LIB3058-039-Q1-K1-F10
US-09-960-352-12673

Query Match 1.98; Score 41.2; DB 10; Length 277;
Best Local Similarity 55.68; Pred. No. 0.21;
Matches 79; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 2057 TTACTCATGTTGTTTGTGATGATCTCGAGCTTTTATGATGTCGAACTGCTGTGCT 2116
DB 258 TTTTCTTTTATTTTATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 199
QY 2117 TTGAGCACCTGTTTGTCTTCAGTGTACTGTCCAGTGTATGCTTTTGACCTTAA 2176
DB 198 TTAATAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 139
QY 2177 AAAAAAAAAAAAAAAAAAAAAA 2198
DB 138 AAAAAAAAAAAAAAAAAAAAAA 117

RESULT 5
US-09-925-301-133
; Sequence 133, Application US/09925301
; Patent No. US20020052508A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 133

```
; LENGTH: 1373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (403)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-133
```

Query Match 1.9%; Score 41; DB 10; Length 1373;

Best Local Similarity 55.2%; Pred. No. 0.72; Mismatches 65; Indels 0; Gaps 0;

```
Matches 80; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 2054 TTATTACTCATGCTTTTGTGATGATCGAGCTTTTGTAGTGTGGAAGTGCCTGT 2113
    || || || || || || || || || || || || || || || || || || || ||
DB 1219 TTGTATTATTAATTTGCTTTGGTATGATTAATGATGATGATGATGATGATGAT 1278

QY 2114 GCTTTGAGCAGCTGTTTATGCTTCAGTGTACTGTCCAGTGTGTTATGCTTTGACCTCT 2173
    || || || || || || || || || || || || || || || || || || || ||
DB 1279 TGTGGGTGCTCTGTGGGCGCATCAATAAAGCCGCTCTGATTTATTTTCAAAAAA 1338

QY 2174 AAAAAAAAAAAAAAAAAAAAAA 2198
    || || || || || || || || || || || || || || || || || || || ||
DB 1339 AAAAAAAAAAAAAAAAAAAAAA 1363
```

RESULT 6

```
US-09-925-302-245
; Sequence 245, Application US/09925302
; Patent No.: US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 245
; LENGTH: 4065
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-302-245
```

Query Match 1.9%; Score 41; DB 10; Length 4065;

Best Local Similarity 50.8%; Pred. No. 1.5; Mismatches 95; Indels 0; Gaps 0;

```
Matches 98; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 2006 TGAAGAACTGAATCTAATAGAGATCAGATGTTTCACTCAGACACATTAATCTTCAT 2055
    || || || || || || || || || || || || || || || || || || || ||
DB 3853 TCAACCATCTAATCTAATAGATTTTGTCTCTGTTCAACACAGTGTATACAG 3912

QY 2066 GTTGTATGATGATCGAGCTTTTGTAGTGTGAACTGCCCTGTTGAGCACC 2125
    || || || || || || || || || || || || || || || || || || || ||
DB 3913 AAATACAGTACGTTCTTCTCTGTGTGTAAGTAATGATGATGATGATGATGATGAT 3972

QY 2126 TGTATTGCTTCACTGTTACTGTCCAGTGTGTTATGTTTGAACCTTAATAAAAAA 2185
    || || || || || || || || || || || || || || || || || || || ||
DB 3973 TGTATTGATCAATTAACACTTAAGAAATTAACATTCCTTTAAAAA 4032

QY 2186 AAAAAAAAAAAAAA 2198
    || || || || || || || || || || || || || || || || || || || ||
DB 4033 AAAAAAAAAAAAAA 4045
```

RESULT 7

```
US-10-123-155-412
; Sequence 412, Application US/10123155
; Publication No. US20030068794A1
```

GENERAL INFORMATION:

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Zhang, Zemin
```

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FILE REFERENCE: P330R1C30

CURRENT APPLICATION NUMBER: US/10/123,155

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 412

LENGTH: 1184

TYPE: PRT

ORGANISM: Homo Sapien

US-10-123-155-412

Query Match 1.8%; Score 40.2; DB 9; Length 1184;

Best Local Similarity 8.5%; Pred. No. 1.1; Mismatches 419; Indels 0; Gaps 0;

```
Matches 56; Conservative 186; Mismatches 419; Indels 0; Gaps 0;

QY 882 TTTCATTTCAATTTGCTGCTCGAATTTCCGTTGCAAGCTTTGAGCCCTTGAAAA 941
    || || || || || || || || || || || || || || || || || || || ||
DB 249 TPKLLTGDSDGRPRIPCLCPDGKSLIKITVVKFAPVILTPKTSLKATIKAEFVR 308

QY 942 ATCAACATCAAAATTTGATTTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1001
    || || || || || || || || || || || || || || || || || || || ||
DB 309 PYWVNPETKARRAGQSVSLCKKATGKRPDPKPYFWYHNDTLLDLSKXKHEKLVLR 368

QY 1002 CAAGTGAAGCCCTGGAAGCTCAATTAATTAAGCTTGAAGCTTGAAGCTTGAAGCT 1061
    || || || || || || || || || || || || || || || || || || || ||
DB 369 HQAGEYFKKQSDAGAVKSKAQLIVTASDTPCNPPVESLILPHPCFNATNSFYD 428

QY 1062 AGATTATGTAATCAATTAATTTCCCAATCCCTGTTGTTGTTGTTGTTGTTGTTGTT 1121
    || || || || || || || || || || || || || || || || || || || ||
DB 429 VGRCPVKTCAGQDONGIICRDVONCCGISKTEREIQCSGYTLPTVKAKKSCORCT 488

QY 1122 TGTGCTCCCAATATTTGAGACTTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 1181
    || || || || || || || || || || || || || || || || || || || ||
DB 489 RSIVGRVSAADNDEPMRFGHVYMGNSRVSMYGRFTTLHPDTERLVLFVDRLOKE 548

QY 1182 GATGAGAGATGTTAGTCTGTTGCAAGACCATGATATCTACAGAAATCCCGAAGC 1241
    || || || || || || || || || || || || || || || || || || || ||
DB 549 VNTTKVLFPNKKSAVFEIKMLRKREPTILEAMETNIILPGEVVGDEPMLELPSRSF 608

QY 1242 ATATATCAATCAATTTGAGCTGGAAGTATGAGGTTGATCTGATCTGCTTCAAGCCCTTGT 1301
    || || || || || || || || || || || || || || || || || || || ||
DB 609 YRQNGEPIYGVKASVFLDPRNISTATAQTDLNFIDEDTPLRLRYGMSVDFRDEV 668

QY 1302 GGATATGACACCTGCTGATTCATGCTGCCGCTTTCATTCATTCATTCATTCATTCAT 1361
    || || || || || || || || || || || || || || || || || || || ||
DB 669 TSEPLNAGKRVVHLDSQVKNPEHISTYKILMSLNPDDGLMEEBGFENORRNKRRED 728

QY 1362 AGAGAAGAGAATAATATCAACCTTAAGAGAGCTGCTTGAAGTGCACCTAGAGGCC 1421
    || || || || || || || || || || || || || || || || || || || ||
DB 729 FLVGNLEIRERKRLNLDVPESRCFVKVRAISRERFLPSBDIQGVISVILBERTGLS 788

QY 1422 AGAAACGTAATATATATATATATATATATATATATATATATATATATATATATAT 1481
    || || || || || || || || || || || || || || || || || || || ||
```

Db 789 NFRANGREDPVTGNGACVPAFCDDSDPAYSAVILASLAGEELQAVESSEKPNMAIG 848
QY 1482 CCTGAGCTGTAGCAATTTAACTGATGCTGTGAAGGCTGTGTTTGAAGTTGAC 1541
Db 849 VPQPLNLRNRTRDHPKRYKTAFOISMARPNSENGPIYAEENLRACEAPPS 908
QY 1542 A 1542
Db 909 A 909

RESULT 8
US-09-731-872-43
; Sequence 43, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bouquelere, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US3.REG
; CURRENT APPLICATION NUMBER: US/09/731.872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 43
; LENGTH: 1942
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 334..1551
; NAME/KEY: sig_peptide
; LOCATION: 334..426
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.0554926521937
; OTHER INFORMATION: seq TVFLVLTIGALDLT/VE
US-09-731-872-43

Query Match 1.8%; Score 40.2; DB 10; Length 1942;
Best Local Similarity 47.1%; Pred. No. 1.5;
Matches 123; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 1021 CACTACAAATTAAGCTTGCCTTTGAAATTCGAATGAGGAAGATTATGTAACGAAAA 1080
Db 1276 CAGTATTAAGTTATCCCTAGCTTTGAGATGACAGTTGTGATGACTACATCAGAGAG 1335
QY 1081 TTCTTCCAAATCCCTGTGTGAGAACTGCTGCTGTTGTTGTTGCTCCAAATTTAG 1140
Db 1336 TTCTGAGGCCACCTGAACACTGGGGTAGTCCCTGATATTTACGATATCCCCAGATCACA 1395
QY 1141 GACTTGTCTCTTCTCTGTTCAATTTTACATATTTAAAGATAGAGAGATGTTGAGTCT 1200
Db 1396 GACTGGCTTCCAGATCAAAAGATGCTATTTCTGTATCAATTTTTCACCCCGGAA 1455
QY 1201 GTTGCAAGACCATGAGATATCTAGCAGAAAAATCCCGAGACATATTAATCAATTCAGG 1260
Db 1456 CTGGCAAGTTACATCAGACGACTGATTTGTATGACAGATTTGTATGAGGCTATGTAGAA 1515
QY 1261 TGAAGTATGAGGTCATCT 1281
Db 1516 TGGAACTGGAAGGGTAGATCT 1536

RESULT 9
US-09-764-853-180
; Sequence 180, Application US/09764853
; Patent No. US2002090672A1
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: Patentlin Ver. 2.0
; SEQ ID NO 180
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1446)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-853-180

Query Match 1.8%; Score 39; DB 10; Length 1446;
Best Local Similarity 49.3%; Pred. No. 2.7;
Matches 99; Conservative 1; Mismatches 101; Indels 0; Gaps 0;

QY 1998 ATTGTGAGTGAAGAACTGAATCTAATAGAGATCAGATGTTTACTCAAGACACATTAT 2057
Db 1238 AATAGAGATGATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1297
QY 2058 TACTCATGCTGTTTGTGATGATCTGACCTTTTATAGTCTGGAACTGCTGCTGTT 2117
Db 1298 TTCAATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1357
QY 2118 TGAGCACCCTGTTATGCTTCAGTGTACTGTCCAGTGTATGCTTTTGAACCTTAA 2177
Db 1358 CAGTACCTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1417
QY 2178 AAAAAAAAAAAAAAAAAAAAAA 2198
Db 1418 AAAAAAAAAAAAAAAAAAAAAA 1438

RESULT 10
US-09-764-853-370/c
; Sequence 370, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: Patentlin Ver. 2.0
; SEQ ID NO 370
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-853-370

Query Match 1.8%; Score 39; DB 10; Length 1446;
Best Local Similarity 49.3%; Pred. No. 2.7;
Matches 99; Conservative 1; Mismatches 101; Indels 0; Gaps 0;

QY 1998 ATTGTGAGTGAAGAACTGAATCTAATAGAGATCAGATGTTTACTCAAGACACATTAT 2057
Db 209 AATAGAGATGATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 150
QY 2058 TACTCATGCTGTTTGTGATGATCTGACCTTTTATAGTCTGGAACTGCTGCTGTT 2117
Db 149 TTCAATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 90

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 00:45:31 ; Search time,5603 Seconds

(without alignments)
11416.735 Million cell updates/sec

Title: US-09-913-858a-1

Perfect score: 2198

Sequence: 1 actaactcaacgctgcatl.....aaaaaaaaaaaaaaaaa 2198

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_or:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vit:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2198	100.0	2198	6 AX033383	AX033383 Sequence
2	2191.6	99.7	2198	6 VRA18529	V18529 Vigna radia
3	690	31.4	1508	8 ATH404860	ATH404860 Arabidops
4	690	31.4	1729	8 ATH345084	AJ345084 Arabidops
5	678.8	30.9	1542	8 ATH345085	AJ345085 Arabidops
6	678.8	30.9	1938	8 AY054522	AY054522 Arabidops
7	664.8	30.2	1834	8 ATH404861	ATH404861 Arabidops
8	534	24.3	658	8 MTR416755	AJ416755 Medicago
9	349	15.9	787	8 AF277228	AF277228 Arabidops
10	346	15.7	588	8 AF277229	AF277229 Arabidops
11	209.4	9.5	2069	6 AX105537	AX105537 Sequence
12	209.4	9.5	2124	6 AX105540	AX105540 Sequence
13	209.4	9.5	2165	6 AX105543	AX105543 Sequence
14	209.4	9.5	2232	6 AX105546	AX105546 Sequence
15	209.4	9.5	2808	6 AX105536	AX105536 Sequence
16	209.4	9.5	2863	6 AX105539	AX105539 Sequence
17	209.4	9.5	2904	6 AX105542	AX105542 Sequence
18	209.4	9.5	2971	6 AX105545	AX105545 Sequence
19	209.4	9.5	3714	6 AX105535	AX105535 Sequence
20	178.8	8.1	104679	8 AC011807	AC011807 Arabidops
21	171	7.8	81875	8 AP000419	AP000419 Arabidops
22	155	7.1	89134	2 AP004162	AP004162 Oryza sat
23	155	7.1	141717	2 AP004457	AP004457 Oryza sat
24	105	4.8	1105	6 AX033385	AX033385 Sequence
25	60.2	2.7	1449	8 BVU315848	AJ315848 Beta vulg
26	60	2.7	1630	8 LES313193	AJ313193 Lycopersi
27	54.6	2.5	177674	2 AC127920	AC127920 Rattus no
28	54.6	2.5	190304	2 AC114439	AC114439 Rattus no
29	53.4	2.4	97683	2 AC116548	AC116548 Dictyoste
30	53.4	2.4	234488	2 AC109698	AC109698 Rattus no
31	53	2.4	807	8 MTR416757	AJ416757 Medicago
32	51.8	2.4	188464	9 AC096757	AC096757 Homo sapi
33	50.6	2.3	122160	2 CEN50797	AL731761 Oryza sat
34	50	2.3	1149	3 CEN505020	AL505020 Caenorhab
35	50	2.3	39370	3 AC006674	AC006674 Caenorhab
36	50	2.3	180664	2 AC006706	AC006706 Caenorhab
37	50	2.3	183800	2 AC123118	AC123118 Rattus no
38	49.8	2.3	241109	2 AC121599	AC121599 Mus muscu
39	49.6	2.3	1128	10 AF345993	AF345993 Rattus no
40	49.4	2.2	1182	8 AY026941	AY026941 Arabidops
41	49.4	2.2	1209	8 ATH404862	AJ404862 Arabidops
42	49.4	2.2	56956	2 AC117081	AC117081 Dictyoste
43	49.4	2.2	80413	8 AC021665	AC021665 Arabidops
44	49.2	2.2	1479	6 AX356085	AX356085 Sequence
45	49.2	2.2	2408	9 AK095482	AK095482 Homo sapi

ALIGNMENTS

RESULT 1
AX033383
LOCUS AX033383
DEFINITION Sequence 1 from Patent WO0049153.
ACCESSION AX033383
VERSION AX033383.1 GI:10280157
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 2198)
AUTHORS Altmann,F.
TITLE Fucosyl transferase gene
JOURNAL Patent: WO 0049153-A 1 24-AUG-2000;
ALTMANN FRIEDRICH (AT)

Db 1981 AGTCACAGCTTCTGTATATGAGTGAACAACTGAAATCTAATAGAGATCAGATGTTT 2040
 QY 2041 CACTCAAGACACATTTATTTATCTATGTTTGTTCATGATCGAGCTTTTATGATCTG 2100
 Db 2041 CACTCAAGACACATTTATTTATCTATGTTTGTTCATGATCGAGCTTTTATGATCTG 2100
 QY 2101 GAACGTGCTGTTGTTTGAGACCTGTTATGCTTCACTGTTACTGTCAGTGGTATC 2160
 Db 2101 GAACGTGCTGTTGTTTGAGACCTGTTATGCTTCACTGTTACTGTCAGTGGTATC 2160
 QY 2161 GTTTTGTACCTCTAAAAAATTTTAAAAAATTTTAAAAA 2198
 Db 2161 GTTTTGTACCTCTAAAAAATTTTAAAAAATTTTAAAAA 2198
 RESULT 2
 VRA18529 2198 bp mRNA linear PLN 01-NOV-2001
 LOCUS VRA18529
 DEFINITION Vigna radiata mRNA for alpha-L-3-fucosyltransferase (Fuct c3).
 ACCESSION Y18529
 VERSION Y18529.1 GI:5702038
 KEYWORDS alpha-L-3-fucosyltransferase; fuct gene; GDP-L-Fuc.
 SOURCEmung bean.
 ORGANISMVigna radiata var. radiata
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Vigna.
 REFERENCE 1
 AUTHORSLeiter, H., Mucha, J., Staudacher, E., Grimm, R., Glossl, J. and
 Altmann, F.
 TITLEPurification, cDNA cloning, and expression of GDP-L-Fuc:Asn-1-linked
 JOURNALGlcNAc alpha1,3-fucosyltransferase from mung beans
 MEDLINEJ. Biol. Chem. 274 (31), 21830-21839 (1999)
 PUBMED99348317
 REFERENCE 2 (bases 1 to 2198)
 AUTHORSMucha, J.
 TITLEDirect Submission
 JOURNALSubmitted (10-DEC-1998) J. Mucha, Institut fuer Chemie, Universitaet
 fuer Bodenkultur Wien, Muthgasse 18, 1190 Wien, Austria
 FEATURES
 Source
 1. 2198
 /organism="Vigna radiata var. radiata"
 /db_xref="taxon:3916"
 /issue_type="sprouts"
 211.. 1743
 /gene="fuct"
 211.. 1743
 /gene="fuct"
 /codon_start=1
 /product="Fuct c3 protein"
 /protein_id="CAB52254.1"
 /db_xref="GI:5702038"
 /translating="MMGLTLNLRGSRDGAQODSLVLAAPGNPKRWSNMLPVLV
 VVAIAFLVGRDLMAKNAAMVDSLADFEYSRAVREDDDLGIVASDRSESCE
 WIEREDAVTYSRDESKSEPIFVSGADDEMSVSGCKRFGSGDGRPPAARFLPDSGA
 SIIRSMESAEYVABENNIAMARRGYNIVHTSSSDVPVYFESMAEDMAPVOPKTE
 AALAAAFISNCGARNRFLQALEALEKSNIKIDISYGGCHRRDRVNVKLEKRFSL
 AFENSNEDVETKRFOSLIVAGTPVAVGAPNIDAPSPGSLIHLKEIDVESVAKT
 MRYLANPEAYNOSLRFMYEGSPDSFKALVDMAAVHSCGLCHLAVSREKENNPS
 LKRPPCKCTGPTVYHYVYRERREMESIYRSSNLTLNAVKAAYLVKFTSLNLP
 VKTERPEVIRGSSALKLYKIPIGLQRALTYTFKGDADRSHLENNPYAKFEVI
 FV"
 BASE COUNT 595 a 412 c 516 g 675 t
 ORIGIN
 Query Match 99.7% Score 2191.6; DB 8; Length 2198;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2194; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ACTAATCAAAACGCTGATTTTCTTTTCTTCAGGAGAACCATCCACCATAACAACAA 60

Db 1 ACTAATCAAAACGCTGATTTTCTTTTCTTCAGGAGAACCATCCACCATAACAACAA 60
 QY 61 AAAAAACAAGACAGAGCTGTCTTTTATATGCTTTTCTTTTAAACAAGACCCCA 120
 Db 61 AAAAAACAAGACAGAGCTGTCTTTTATATGCTTTTCTTTTAAACAAGACCCCA 120
 QY 121 TCATGATGCTGTCTATTAACGCCAAATTTCCATTTCCCTTGATTTAGTTATTT 180
 Db 121 TCATGATGCTGTCTATTAACGCCAAATTTCCATTTCCCTTGATTTAGTTATTT 180
 QY 181 TCGGAATTTGGCACTGTGGGGCGCAATTGAATGATGGGTCTGTAGCAATCTTCGAGGC 240
 Db 181 TCGGAATTTGGCACTGTGGGGCGCAATTGAATGATGGGTCTGTAGCAATCTTCGAGGC 240
 QY 241 TCGAGACAGATGGTGGCCCAACAGACAGCTTACCCTTTTGGCTCGGGGAGCAACCA 300
 Db 241 TCGAGACAGATGGTGGCCCAACAGACAGCTTACCCTTTTGGCTCGGGGAGCAACCA 300
 QY 301 AAGAGAAATGAGACCAATCTAATGCTCTTGTGTGTCCTTGGCTATCGCGAGATC 360
 Db 301 AAGAGAAATGAGACCAATCTAATGCTCTTGTGTGTCCTTGGCTATCGCGAGATC 360
 QY 361 GCGTTTCTGGGTAGGTTGATATGGCCAAACAGCCGCATGTTGACTCCCTGCTGAC 420
 Db 361 GCGTTTCTGGGTAGGTTGATATGGCCAAACAGCCGCATGTTGACTCCCTGCTGAC 420
 QY 421 TTCTTCTACCGCTCTCGAGCGGTGTTGAAGTATACCATTTGGGGTGTGGTGGCT 480
 Db 421 TTCTTCTACCGCTCTCGAGCGGTGTTGAAGTATACCATTTGGGGTGTGGTGGCT 480
 QY 481 TCTGATGGAATTTGATCGATCTATAGTTGTGAGAAATGTTGAGAGAGAGATGCTGC 540
 Db 481 TCTGATGGAATTTGATCGATCTATAGTTGTGAGAAATGTTGAGAGAGAGATGCTGC 540
 QY 541 ACGTATTCGAGGGCTTTTCCAAAGAGCTATTTTGTTCGTGAGCTGATCAGAGTGC 600
 Db 541 ACGTATTCGAGGGCTTTTCCAAAGAGCTATTTTGTTCGTGAGCTGATCAGAGTGC 600
 QY 601 AAGCGGTGCTGGGTGGATGTAATTTGGGTTTGTGGGGATAGAAAGCCGATGCCGCA 660
 Db 601 AAGCGGTGCTGGGTGGATGTAATTTGGGTTTGTGGGGATAGAAAGCCGATGCCGCA 660
 QY 661 TTTGGTTCCTCAACCAAGTGAAGAGCTGATTCCTGCGATCAATGATCAGCAGAA 720
 Db 661 TTTGGTTCCTCAACCAAGTGAAGAGCTGATTCCTGCGATCAATGATCAGCAGAA 720
 QY 721 TACTATGCTGAGAACATATTGCAATGAGCAAGAGGAGATTAACATCTAATGACA 780
 Db 721 TACTATGCTGAGAACATATTGCAATGAGCAAGAGGAGATTAACATCTAATGACA 780
 QY 781 ACCAGCTATCTGGGAGATTCCTGTTGGATATTTTTCATGGCTGATGATATGATG 840
 Db 781 ACCAGCTATCTGGGAGATTCCTGTTGGATATTTTTCATGGCTGATGATATGATG 840
 QY 841 GCACAGTCAATTTGGAGATTCCTGTTGGATATTTTTCATGGCTGATGATATGATG 840
 Db 841 GCACAGTCAATTTGGAGATTCCTGTTGGATATTTTTCATGGCTGATGATATGATG 840
 QY 901 GCTGGAATTTCCGTTGCAAGCTCTTGGAGCCCTTGAAATCAAAACATCAAAATTGAT 960
 Db 901 GCTGGAATTTCCGTTGCAAGCTCTTGGAGCCCTTGAAATCAAAACATCAAAATTGAT 960
 QY 961 TCTTATGCTGTTTTCACAGAACCCGATGATGAGAGAGTGAAGCAAGTGGAGCCCTGAG 1020
 Db 961 TCTTATGCTGTTTTCACAGAACCCGATGATGAGAGAGTGAAGCAAGTGGAGCCCTGAG 1020
 QY 1021 CACTACAATTTAGCTTAGCTTTGAAATTCGATGAGAGATTAATGTAATGAAATA 1080
 Db 1021 CACTACAATTTAGCTTAGCTTTGAAATTCGATGAGAGATTAATGTAATGAAATA 1080
 QY 1081 TTCTTCAATCCCTGTTGCTGGAACCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1140
 Db 1081 TTCTTCAATCCCTGTTGCTGGAACCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1140

[illegible]

RESULT 3	
LOCUS	ATHA04860
DEFINITION	ATHA04860 1506 bp mRNA linear PLN 25-JUN-2001 Arabidopsis thaliana mRNA for alpha,3-fucosyltransferase (FUCTA gene).
ACCESSION	At404860
VERSION	At404860.1 GI:13992482
KEYWORDS	alpha 1,3-fucosyltransferase; FUCTA gene.
SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 1506)
AUTHORS	Wilson,I.B., Rendic,D., Freilinger,A., Dunic,J., Altmann,F., Mueha,J., Muller,S. and Hauser,M.T.
TITLE	Cloning and expression of cDNAs encoding alpha1,3-fucosyltransferase homologues from Arabidopsis thaliana
JOURNAL	Biochim. Biophys. Acta 1527 (1-2), 88-96 (2001)
MEDLINE	21313304
PUBMED	11420147
REFERENCE	2 (bases 1 to 1506)
AUTHORS	Wilson,I.B.H.
TITLE	Direct Submission
JOURNAL	Submitted (11-Jul-2000) Wilson I.B.H., Institut fuer Chemie, Universitaet fuer Bodenkultur, Muthgasse 10, Wien 1190, Austria
FEATURES	Location/Qualifiers

source	gene	CDS	BASE COUNT
1..1506			413 a
/organism="Arabidopsis thaliana"			304 c
/strain="Columbia"			344 g
/db_xref="taxon:3702"			445 t
1..1506			
/gene="FucTA"			
1..1506			
/gene="FucTA"			
/function="glycosyltransferase: fucose transfer"			
/codon_start=1			
/product="alpha1,3-fucosyltransferase"			
/protein_id="CAC38048.1"			
/db_xref="GI:13992483"			
/translation="MGVESSLRGPKIGLTHELPELVANGSTSSSSPSPFKRVSTF			
PICVALVIIEIGFLCDLNASLVDTHLFTKSSDLKVSQGLKEQEWLEIRDSVY			
YSRPYKDPRTIFSSNKKDFKSCSYDCVWGFISSDKRPDAEBSLHQPTLSLRMSYS			
QYIOENNDAQRRKRGYDITVMTTSLSSDVPVGFESMAEYDIAVPQPTERKALAAAFIS			
NCAARFLQALALELMTKNKIDSYGCHRRDSSVEKVALIKYKFSLAETNNDEE			
YVTKFQPSILVAGSVPVVGCAPINIEEFAFSPDSFLHIKOMDVAVAKMKMYLADNDEE			
AYNTLRMKHGGSPFKALIDMAAVHSSCRCLFVATRIREEOKSPEEFRRCKCT			
RGSSTVYHLYVREGRFDMESILFLKDGSLTLEALSVAIAKEMSLRAYEPIWKRRPAS			
LRGGSKLRVHGYIPIGLTORALYNFKFEFGNSSLTHIQRNCPKFEVVFV"			

[illegible]

QY	733	AACATATTTGGCATGCGACAGACGAGGGGATATTAACATCGTAATGACAAACCACTATCT	792
Db	496	AATATATCTTGCTCAAGCAGCAGCAAGAAAGTTATGATATTTGATGACAACTAGTCTGCA	555
QY	793	TGCGATGTTCTGTGGATATTTTTTCATGGGCTGATGATGATGATGAGGACCAAGTGCAG	852
Db	556	TCGATGTCTGTGGGATATTTTTTCATGGGCGGAATATGATATTAATGATGCTCCAGTGC	615
QY	853	CCGAAACTGGAAGCTGCTTCGACGCTTCATTTCCATTTGTTGGTGCACGAATTC	912
Db	616	CCAAAAACAGAAAGCTCTGTGCTGCTTTTATTTCCAAATTCGCGCGGAAATTC	675
QY	913	CGTTGCAAGCTCTTTGAGGGCCCTGAAAAATCAAAACATCAAAATTTGATCTTAATG	972
Db	676	CGCCTGCAAGCTCTTTGAAGCCTTAATGAAGACGAATGTAAGATTGATCTTAATG	735
QY	973	TGTCACAGGAACCGTATGGAAGAGTACAAAGTGCAGCCCTGAGACCTACAAATTT	1032
Db	736	TGTACCGGAATCGGAGGGAGGTGTGGAAGGTGAAGCTTTAAACCTACAAATTC	795
QY	1033	AGCTTACGCTTTGAAAAATTCGAATGAGGAATTAATGAATCGAAAAATTTCTCCAAATC	1092
Db	796	AGTCTAGCTTTTGAAGAACCAACAGAGAGGATTAATGTCACAGAGAAGTTCTTCCAACT	855
QY	1093	CTTGTGTGCTGGAACCTGTCCTGTGTGTGTTGGTGTGCTCCAAATATTGAGACTTTGCTCT	1152
Db	856	CTAATCGCTGATCTGTCCTGTGTGTGTTGGAGCTCCAAATATTGAGAAATTTGACCT	915
QY	1153	TCCTCTGCTTCAATTTTATCATATTAAGAAGATTAAGAGATGTTGAGTCTGTGCAAAAGC	1212
Db	916	TCCTCTGCTTCAATTTTATCATATTAAGAAGATTAAGAGATGTTGAGTCTGTGCAAAAGAA	975
QY	1213	ATGAGATATCTAGCAGAGAAAAATCCCGAAGCATATATCATCATTTGAGAGTGAAGATTAAG	1272
Db	976	ATGAAGATCTTTGGGGATTAACCCCTGAGCCCTTAATATCAGAGGCTTAAGATGGAACATGAA	1035
QY	1273	GGTCATCTGACTCTCTTAAGGCCCTTGATGATGCGTGTGCTATTCCTGTCCTG	1332
Db	1036	GGCCCTTACAGATTTCTTTTAAAGCACTTAATGATATGGCTGTGACACTCTTCTGTGCT	1095
QY	1333	CTTTGCAATTCAGTTGGCCACAGTGAAGTGAAGAAAGAAATTAATCCAAAGCCTTAAG	1392
Db	1096	CTCTGCAATCTTTGTGCTTACAAAGATTTGCTGAACAGAAAGAAAGAGCCCTGAGTTTAAG	1155
QY	1393	AGACGTCTTTCAGTGAAGTGCATGAGGGCCAGAAAACCGTATATCATATCTATGTCAGAAA	1452
Db	1156	AGACGACCCCTCAAAATGACACAGAGGCTCAAGAGACAGTTTATCATTTGTATGTTAGAAA	1215
QY	1453	AGGGGAAGCTTGAAGTGAATGCCATTTACTGAGAGTGTACGAATTTAACTCTGATGCT	1512
Db	1216	AGAGAGACGGTTTGAATGGAATCCATCTTTTGAAGATGGAATACTCATCTGGAACCT	1275
QY	1513	GTGAAGGCTGCTGTGTTTAAAGTTCATCCCTGATCTTGTGCTGTATGGAAGACT	1572
Db	1276	CTGGAATGTGGGTTGCTTGGCAAGTTCATGCTGTGATATGAAACCAATATGGAAGAG	1335
QY	1573	GAAAGCCTGAAGTTATTAAGAGGGGGAGTCTTTAAACTCTACAAATATACCAATT	1632
Db	1336	GAAAGACCCCGAGCTTAAGAGGAGACCGCAAGCTTTAAGATACATGGGATATATCTTATT	1395
QY	1633	GGCTTGAACACAGAGACGCTTTTATATCTTTACCTCTTCAAGAGGATGAGCTTACG	1692
Db	1396	GGTCTGACTCAAAAGCAAGCTCTTTTACAATCTTCAAAATTTGGAAGCAATTCAGACTTCACT	1455
QY	1693	AGTCACTTGGAACCAATCTGTGCCAAGTTTGAAGTCAATTTTGTGTGTA	1742
Db	1456	ACTCACATACAGAGAAACCTTGTGCCAAATTCGAAGTTGTCTTGTGCTGA	1505

DEFINITION	Accession	Version	Keywords	Source	Organism	Reference	Authors	Title
Arabidopsis thaliana mRNA for core-alpha1,3fucosyltransferase 1 (fuc1 gene).	AJ345084							
core-alpha1,3fucosyltransferase 1; fuc1 gene.	AJ345084.1	GI:15722479						
thale cress.								
Arabidopsis thaliana								
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots: Rosidae: eurosids II; Brassicales; Brassicaceae; Arabidopsis.								
1 (bases 1 to 1729)								
Bakker, H.								
Molecular cloning and characterization of a plant (beta vulgaris)alpha1,4-fucosyltransferase with specificity for Lewisia and Lewis synthesis								
Unpublished								
2 (bases 1 to 1729)								
Bakker, H.								
Direct Submission								
Submitted (14-SEP-2001) Bakker H., Plant Research International, Wageningen University and Research center, droevendaalsesteeg 1, Netherlands 6708PB, NETHERLANDS								
Location/Qualifiers								
1..1729								
/organism="Arabidopsis thaliana"								
/variety="Colombia"								
/db_xref="taxon:3702"								
/tissue_lib="selique"								
93..1598								
/gene="fuc1"								
93..1598								
/gene="fuc1"								
/function="glycosyltransferase involved in N-glycan biosynthesis"								
/codon_start=1								
/product="core-alpha1,3fucosyltransferase 1"								
/protein_id="CAC78979.1"								
/db_xref="GI:15722480"								
/translation="MGVFNLSRGKIGLTHEELPVANGSTSSSSSPSRKYSTFLPICVALVIEIGLICLDNLSAVDTLTFHTKSSDCLKVSGIEKQCEMLERDSVTLYSRFETKDFIFSGSNKDFSCSVDCGPGVSPDKPAAGLSHGPGLTSLIRMSASAYOEENLAAARRGVDIVMTTSLSPVGPFSMAVDIMAPVQPTETALAAFTISNCARNRFDLALEMAKTINRKIDSYGGCHNRDGSYKVELKIKYSLAFENTNEEDYVEKFPKSLVAGSVPVVAGAPNIEEPSPDSFLHKQMDVAANKKRYLDNDFAYNQTFLRKHGSPDSFKALIDMAVHSSCLCFVATRIREDKSPERKRPCKCTRGSTVYHLVYERKGRDMSIFLKDNLTEALEASVLAKFMSLRPELTKERPARSLRGGRVLRHGIYPIGLTORALVLPFEKSGSLSTHIOBNPCPKFVFEV"								
BASE COUNT	508 a	333 c	374 g	514 t				
ORIGIN								
Query Match	31.4%	Score 690;	DB 8;	Length 1729;				
Best Local Similarity	72.0%	Pred. No. 7.4e-165;						
Matches 900; Conservative	0;	Mismatches 350;	Indels	0;	Gaps	0;		
493	TCTGAATCGTATAGTTGGAGAAATGTTGGAGAGGAGAAATGCTGCACGATTCGAGG	552						
348	TCAGGAATAGAGAAATGCCAGAGAGTGTAGAGAGTGGATTCAGTTACTTATTTCTGA	407						
553	GGCTTTTCCAAAGAGCCATATTTTGTCTTGAGCTGATCAGAGAGTGGAGTGGTTCG	612						
408	GATTTCACTAAGAATCCGATTTTATCTCTGTAGTACTACAAAGAGCTCAAAATCGCTCT	467						
613	GTTGATGATTAATTTGGGTTTAGTGGGATGAAGAAGCCAGATCCCGCATTTGGTTACT	672						
468	GTTGATTTGTGAATGGGATTCACATTCAGATGAAGAAACCTGATGGCTTTGGATTAAAGT	527						
673	CAACCAAGTGGAGACAGTACGATTCCTCGGATCAATGATGATAGCAGATACTATCTGAG	732						
528	CATCACTGGAACACCTGATATATATCGCTTCATGATGATACGACACAGATATTACCAAG	587						
733	AACATATTCGCATGCGACAGACGAGGGGATATTAACATCGTATATGACAAACAGTATCT	792						
588	AATATCTTGTCTCAAGCAGCAGGAAAGTATATGATTTGGATGATCAACATAGTCTGCA	647						

LOCUS	DEFINITION	ACCESSION	VERSION
ATH345085	Arabidopsis thaliana mRNA for core-alpha1, 3fucosyltransferase 2 (fucT2 gene).	AJ345085.1	GI:15722481
Db	648	TCAGATGTTCTCTTGGGTAATTTTTCATGCGCGGATATGATATTTATGGCTCCAGTGCAA	707
Qy	853	CCGAAACTGAAGCTGCTCTTGACGTGCTTCATTCCCAATTTGTTGTCCTGAAATTTTC	912
Db	708	CCAAAAACGAGAAAGAGCTCTGCTGCTGCTTATTTATTTCCAAATTTGCGCCCTGGAAATTC	767
Qy	913	CGGTTGCAAGCTCTTGAGGCCCTTGAAAAATCAACATCAAAATTCATTCTTATGGTGGT	972
Db	768	CGCTCGCAAGCTCTTGAACCTTATGAAGAGGAATGTTAAATGATTTGATTCTTAAGTGGT	827
Qy	973	TGTCAAGAGAACCGTGATGAGAGCAAGCAAGTGAAGCCCTGAGCAGCTACAAATTT	1032
Db	828	TGTCAACCGGAATTCGGATGTGGAGTGTGGAGAAAGTTGAAGCTCTTAAGCACTACAAATTC	887
Qy	1033	ACCTTAGCTTTGAAATATCGAATGAGAAATTTATTAAGTGAATAATTTCTTCACATCC	1092
Db	888	ACCTTAGCTTTTGAAGAACCAACGAGGGAGATTTATGTCACAGAGAAATTTCTTCACATCT	947
Qy	1093	CTTGTTGCTGGAACGTGCTGCGTGGTGTGGAGTGGTCCAAATTTTCAGGACTTTGGTCTCT	1152
Db	948	CTAAGTGGCTGGAATCTGTCCCTGTGGTGTGGAGCTCCAAATTTAGAAATTTTGACCT	1007
Qy	1153	TCTCTGTGTTCAATTTTACATATTAAGAGATAGAGAGTGTGAGTCTGTCCAAAGACC	1212
Db	1008	TCTCTGACTCATTTCTCTTCATCAATTAAGCAGATGATGATGTCAGGCAATTTCCAAAGAAA	1067
Qy	1213	ATGACATATCTTAGCAGAAATATCCGAGACATATTAATCAATCATTTGAGTGGAGATAGAG	1272
Db	1068	ATGAAGTATCTTGGCGATTAACCTCTGCGCTTAAATCAACACCTTAAGATGAGAAACATGAA	1127
Qy	1273	GGTCAATCTGACCTCTTCAAGGCCCTGTGGATATGGACGCTGTGATTCATTCGTCGCT	1332
Db	1128	GGCCCTTCAGATTTCTTTTAGGCACTTATGTATATGGCTGTGTACACTCTTCTGTGCT	1187
Qy	1333	CTTTCATTTCAACTTGGCCACAGTGAATGAGAGAGAGAAATTAATCCAGCCTTTAG	1392
Db	1188	CTCTGATCTTCTTGTGGCTACAGAGATTTGTGTGAGCAAGAGAGAGCCCTGATTTAG	1247
Qy	1393	AGACGTCCTTGAAGTGCACGTAGAGGGCCAGAAACCGTATATCATATCTATGTACAGAA	1452
Db	1248	AGACGACCTCTGGAATATGACCCAGAGCTCAGAGACAGTTATTCATTGTATGTTAGAGAA	1307
Qy	1453	AGGGAAGGTTTGAATGAGTGAATTCATTTACCTGAGGCTTACCAATTTTATCTGTGATGCT	1512
Db	1308	AGAGGACGGTTTGAATGAGTAATCCATCTTCTTGAAGAGATGAAATCTGACTGTGAACT	1367
Qy	1513	GTGAAGGCTGCTGTTGTTTGAAGTTACATCCCTGAATCTTGTGCTGTATGGAAGACT	1572
Db	1368	CTGGAATCTGCGGTTCTTCTCCGAAGTTCAATGCTGTGATGATGAACCAATATGGAAGAG	1427
Qy	1573	GAAAGGCTTGAAGTATTAAGAGGGGGAGTGTCTTTAAACTCTACAAAATATATACCAAT	1632
Db	1428	GAAAGACCCCGGAGCTTAAAGAGGAACGGCAAGCTTAGAGTACATGGGATATATATCTTAT	1487
Qy	1633	GGCTTGACACAGAGCAAGCTCTTATATACCTTCAGCTTCAAGGATGATCTGATTTCAAG	1692
Db	1488	GGTGTACCTCAAGACAAAGCTCTTTTACCACTTCAATTTTGAAGGAATTTCAAGTCTCAGT	1547
Qy	1693	AGTCACTTGGAGAACATCTTGTGCCAAGTTTGAAGTCAATTTTGTGTGA	1742
Db	1548	ACTCACTATGAGAGAAACCTTGTCCCAATTCGAAGTGTCTTTGTGTGA	1597

KEYWORDS	core-alpha1,3fucosyltransferase 2; fucT2 gene.
SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS	Bakker, H.
TITLE	Molecular cloning and characterization of a plant (Beta vulgaris)alpha1,4-fucosyltransferase with specificity for Lewis and LewisX synthesis
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1542)
AUTHORS	Bakker, H.
TITLE	Direct Submission
JOURNAL	Submitted (14-SEP-2001) Bakker H., Plant Research International, Wageningen University and Research centre, droevendaalsesteeg 1, Netherlands 6708PB, NETHERLANDS
FEATURES	Location/Qualifiers
source	1..1542
	/organism="Arabidopsis thaliana"
	/variety="colombia"
	/db_xref="taxon:3702"
	/tissue_type="selique"
gene	1..1542
	/gene="fucT2"
	1..1542
	/gene="fucT2"
	/function="glycosyltransferase involved in N-glycan biosynthesis"
	/codon_start=1
	/product="core-alpha1,3fucosyltransferase 2"
	/protein_id="CA078980.1"
	/db_xref="GI:15722482"
	/translation="MGVSNLRGPRAGATHDEPATNPGSSSSSSSIKRKLNLNLIPLCALVYIAIEIGFLRDLKALVDITDDEFTQSPUSQSPPARSDRKIGLFDPSRSEMLMREDSVYSRDPDKDPEIIGSGDEDFQMCVDCPFGSSSKTPDAAGCLOKRS
	TLSTIRSMESQIYIPENDLAARRGDIYVTTLSISDVPIGYSMAETDIMEFOPPT
	TERIAAFAISNGARNFRLOALEALMTNTRKIDSYGGRNRGKVDKVALRYRKE
	SLAENENEDYVTEKEPFOSLVAGSVPVVGPPIEERPAVSDSLFKTKTDEVEPAV
	KRMVFLAANPAAYNOTLRMKYEGPDSDFKALVDMAAVSSCRLCIFLATRVDEEES
	PNFKRPPCKCRGSGSDIYVHVEVERGEFEMESVFLRKSSTOEALESAVLAKRSLK
	HEAVMKRERPNLKGDKELKIHRIYPIGLTRQALYNKRFEGNSLSLHINPCKAKK
	EYVYV"
BASE COUNT	423 a 302 c 370 g 447 t
ORIGIN	
Query Match	30.9%; Score 678.8; DB 8; Length 1542;
Best Local Similarity	68.4%; Pred. No. 5.3e-162;
Matches	989; Conservative 0; Mismatches 442; Indels 15; Gaps 3;
0Y	301 AAGAGGAATGAGCAATCTAATGCCCTCTGTTGTCGCCCTTGCGTATCGCGGAGATC 360
Db	109 AAGCGAAATTTGCAAAATTTGTACCACTCGCGTTGCTCTGTGATTATCGCTGAGATC 168
0Y	361 GCGTTTCGGGAGAGTGGATATGCGCAAAAGCGCGCGCATGGTGACATCCCTCGGTGC 420
Db	169 GGGTTTCTGGGTGGCGCTCAT-----AAAGTCGCTTTGGTTGATACGTTGACTCAT 219
0Y	421 TTTCTTACCCGCTCTGAGACCGGTGCTTGAAGGTGACGATTGGGGGTGGTTGGTGCT 480
Db	220 TTTCTTACCCCACTCTCCGTCACCTCTCGCAGTCTCCACCGCGAGATCCGATCGGAAGA 279
0Y	481 TCTGATCGGAATTCGATCATGATAGTTGTGAGGAATGTTGGAAGAGGAGATGCTGTC 540
Db	280 ATCGGATTAATTACGATAGG--AGTCGCGAGGAGTGGTATGAGAAATATTCAGATT 336
0Y	541 ACGTATTGAGAGGCGTTTCCCAAGAGCGCTATTGTTGTTTCGAGACGATCAGAGGTGG 600
Db	337 ACTTACTCTAGAGATTTTACTTAAGATCCAAATTTTATCTCTCGTGGTGGTAAAGACATT 396
0Y	601 AAGTCGTGTGGGTGATGTAATTTGGGTTTAAGTGGGGATAGAAAGCCAGATGCCCA 660

D	b	397	CAGGGGTCTGTGAGATTGTACATTTGGAGATAGTTGAGGAAAAACACAGATGCTGG	456
O	y	661	TTTGGGTACCTCAACCAAGTGGACAGCTAGCATTTCTGCATCATGGATCAGCAGAA	720
D	b	457	TTTGGATTAGGTGAGAAACCTGGAACTCTTAGTAATAATACGTTCCATGGAAATCAGACAG	516
O	y	721	TACATGCTGAGAAACAATATGGCATGGCAACGAGGGGATATACATGCTAATGCA	780
D	b	517	TATTATCCAGAAAATGTCTTGCACAGGCACACGAGGGGTTATGATATATGTATGACC	576
O	y	781	ACCAAGTATCTTGGATGTTCCCTGTGGATATATTTTCATGGGCTAGATAGATATG	840
D	b	577	ACTATGCTATCATCATAGATGTCTCTGTGGATATTTTCTGTGGCGAGATGATATTTAG	636
O	y	841	GCACCAAGTCAGCCGAAAAACCTGAAGCTGCTTTGCAGCTCTTTCATTTCCAAATTTG	900
D	b	637	TCCTCCGGTACAGCCAAAACCTGAGAGCATATATGACAGCTTTTATTCTAATTTGTG	696
O	y	901	GCCTGAATTTCCGGTTGCAAGCTCTTGAGGCCCTTGAAAATCAACATCAAAATTTGAT	960
D	b	697	GCCTGGAAATTTTGGCTACACAGCATTTGAGCATATGATGAAAACATCAATTAAGTTGAT	756
O	y	961	TCCTATGTTGGTTGTACACAGAACCGTGTATGAGAGGTAAACAAAGTGGAAACCTTAAG	1020
D	b	757	TCTTATGTTGGTTGTCTATCGAAACCGGATGGGAAAGTTGACAAAGTTGAAGCTTTAAG	816
O	y	1021	CACATCAAAATTTAGCTTAGCTTAGCAATTTGCAATGAGGAAGATTATGTAACTGAAAAA	1080
D	b	817	CGATCAAAATTTAGTTGGCTTTTGGAAATACAAAGGAAGATTATGTACCGAGAA	876
O	y	1081	TTCTTCCAAATCCCTGTGTGTGGAACCTGTCTGTGTGTTGTGTCTCAATATTTAG	1140
D	b	877	TTCTTTAAATCTTAGTGTGTGGGTCGGTCCCGGCGTGATGTGGCTCTCCAAATTTAATA	936
O	y	1141	GACTTCTCTCTCTCTCTCTGTTCAATTTTACATATTAAGATFAGAGATTTGAGCT	1200
D	b	937	GAATTTGGCGCTGTGTGACATATCTTTCACATTATACATATGGAAGATGTAGACCA	996
O	y	1201	GTTGCAAAAGCACATGAGATATCTAGCAGAAAATCCCGAAGCATATATCATCATTTGAG	1260
D	b	997	GTTTCCAAGGAATTAAGATATCTGCGACGTAAACCCGTGCTTATATACAGACACTAGA	1056
O	y	1261	TGGAAGTATAGGGTCCATCTGATCTGCTTCAGAGCCCTGTGTGATATGGCAGCTGTGAT	1320
D	b	1057	TGGAATATCAGAGGGTCCCTAGATTTTTCACAGCAGCTTTGTAATATGGCTGTGTAC	1116
O	y	1321	TCATCTGTCGCTCTTTCATCTACTTCTGCGACAGTAGTAGAGAGAGAGAAAAATAT	1380
D	b	1117	TCCTTCTGGCGTCTCTGATTTCTTCTGCGCAGAGGGTCCGAAACAGAGAGAAAAGC	1176
O	y	1381	CCAAGCCTTAGAGAGCGTCCCTGCAAGT--GCATAGAGGGGCCAGAAAACCGTATATCAT	1437
D	b	1177	CCTAATTTCAAGAAACGACCGCTCAATATGAGCAGGGAGATCAGACACAGTTATCAT	1236
O	y	1438	ATCATATGTCAGAAAGGGAGAGTTTGAGATGAGTCCATTTTACCTAGAGCTTAGCAT	1497
D	b	1237	GTTTTTTGTAGAGAAAGGCGGTTTGAATGTAGTCTTTTGGAGGGGTAAAAAT	1296
O	y	1498	TTAATCTGATGCTGTGAGGGCGGTGTTTGAATTCACATCCCTGATATCTTG	1557
D	b	1297	GTGACTCAGAGAGCTCTAGATATTCGAGATTTCTGCCAATTCAGCTTTTAAACATAG	1366
O	y	1558	CCTGATAGAGAGTGAAGAGCCTGAAGTTATTAAGAGGGGAGAGTCTTAAACCTTAC	1617
D	b	1357	GCAGTGTGAAGAAAGAAAGGCTCGAAACTTAAAGGAGACAAAGAGCTTAAATATCAT	1416
O	y	1618	AAAAATATACCAATTTGGCTTGACACAGAGACAGCTCTTTATACCTCAGCTTCAAAGT	1677
D	b	1417	CGGATTTACCGGCTTGGCCTTACGCAACGACAGGCTTGTACAACTTCAAATTCAGAGGA	1476
O	y	1678	GATGCTATTTTCAGAGAGTCACTTGGAGAACAAATCCTTTGGCCAAAGTTGAATCATTTTT	1737
D	b	1477	AATTCAGCTCTAAGTATCTCATTTCAAACACACCTTTGGCTTAATTTAGAGTTCTCTTC	1536

QY	1738	GTGTAG	1743
Db	1537	GTCTAG	1542

RESULT 6	AY054522	1938 bp	mRNA	linear	PLN 05-SEP-2001
LOCUS	AY054522				
DEFINITION	Arabidopsis thaliana Putative fucosyltransferase (AtUGT9710);				
ACCESSION	AY054522				
VERSION	AY054522.1				
KEYWORDS	FUT-CDNA.				
SOURCE	Arabidopsis thaliana.				
ORGANISM	Arabidopsis thaliana				

	misc_feature	73..1618	30.2%: Score 664.8: DB 8: Length 1834;
	Query Match	30.2%: Score 664.8: DB 8: Length 1834;	
	Best Local Similarity	68.2%: Pred. NO. 2e-158;	
	Matches 989: Conservative	0: Mismatches 442: Indels 19: Gaps 4:	
	BASE COUNT	509 a 358 c 422 g 545 t	
	ORIGIN		
QY	301	AAGAGAAATGAGACATCTAATGACCTCTGTTGTCGCCCTGTGTGATCGCGAGATC	360
DB	178	AAGGAAAATTAATGCAATTTGTTACACTGCGCTGCTGTGTAGTTATCGCTAGATC	237
QY	361	CGCTTCTGTGGTAGTGGATATGCGCCAAAACGCCGCCATGCTGACTCCCTCGCTGAC	420
DB	238	GGGTTTCTGGGTCGGCTCGAT-----AAAGTCGCTTTGGTGAATACGTTGACTGAT	288
QY	421	TTCTTCACCCGCTCGACGCGGTGGTTGAAGTGAACATTTGGGTTGGTTGGTGGCT	480
DB	289	TTCTTCACCCAGCTCCGCTCACTCTCGCACTCTCCACCGCGAGATCCGATCGAAGAG	348
QY	481	TCGTATCGGAATTTCTGAATTCGTATAGTTGTGAGAAATGTTGAAGAGAGATCTGTC	540
DB	349	ATCGGATTAATTTACTGATAGG---AGCGGAGAGAGTGGTTGATAGAGAAATTCAGTT	405
QY	541	ACGATTTGAGAGGGCTTTTCCAAAGAGCCATATTTTGTTCCTGAGCTGATCAGAGTGG	600
DB	406	ACTTACTCTAGAGATTTTACTAAAGATCCAAATTTTATCTCGTGCGTGAAGAAAGACTTT	465
QY	601	AAGTGTGTGGGTGGAGTGAATATTTGGGTTTACTGGGGATAGAAAGCAATGCCGA	660
DB	466	CAATGCTTTCTGTGGATTTGATCTTGGAGTACTTCAAGGGAACACCGAGATCTGCG	525
QY	661	TTTGGGTACCTCAACCAAGTGAACAGCTAGACATTTCTGCAATCAATGAAATCAGACAGA	720
DB	526	TTTGGATTAAGTCAAAACCTGGAAGCTCTTACTATAATACGTTCCATGTAATCAGACAG	585
QY	721	TACTATGCTGAGACAATATTTGCCATGGCAGACGGAGG---GGATATACATCGTAAT	776
DB	586	TATATTCAGAAAAATGATCTTGCACAGCACACCGGTGGAGAGGTTATGATATATGAT	645
QY	777	GACACCAAGTCATCTTGGATGTCCTGTGGATATTTTATAGGGCTGATATGATAT	836
DB	646	GACCACTAGTCTATCATCAGATGCTCTGTGGATATTTTGTGGCGCGATAGATATAT	705
QY	837	GATGACACAGTGCAGCGGAAGTGAAGCTCTCTTGGAGCTGGTTTATTTCCAAATG	896
DB	706	TATGCTCCGGTACAGCCAAAACGAGAGAGCTATGAGCTGCTTTTATTTCTAATTG	765
QY	897	TGTGCTCGAAATTTCCGGTGTGCAAGCTCTTGAGGCCCTTGAATAATCAACATCAAAAT	956
DB	766	TGTGCTCGGAATTTTTCGTCACAGCACTTGAGGCATGATGAATAACTAATCAATTAAGAT	825
QY	957	TGATCTTATGTTGTTGTACAGAACCCGTATGGAAGCTGAACCAAGTGAAGCCCT	1016
DB	826	TGATCTTATGTTGTTGTACAGAACCCGGATGGGAAGCTGCAAGGTGAAGCTCT	885
QY	1017	GAAGCACTACAAATTTAGCTTAGCTTTGAAATTCGAATGAGGAAGATATATTAACCTA	1076
DB	886	TAAAGCATACAAATTTCACTTTGGCTTTTGAGATACATAACGAGGAAGATATATGACCGA	945
QY	1077	AAAAATCTTCCAAATCCCTGTGTGCTGGAACGTCCCTGTGTGTGTGTGCTCCAAATAT	1136
DB	946	GAAGTTCTTCAATCTTATGTTGCTGGGCGGTCGCCGCGTGGTGGTCCCAATAT	1005
QY	1137	TCAGACATTTGCTCTTCTCCGTGTTCAATTTTACATATTAAGAGATAGAGAGTGTGA	1196
DB	1006	AGAAATTTTGGCGCTGCTCGACTCAATCTCTTACATTAAGACTATGAGAGATGTAGA	1065
QY	1197	GTCGTTGCAAAAGACATGAGATATCTGACAGAAATCCCGAAGATATATCAATCAAT	1256
DB	1066	GCCACTTTCAAAAGAAATGAGATATCTGACAGCTAACCTGCTGCTTATATACAGACT	1125

OY	1257	GAGGGGAAGAATGATGAGGGGTCCATCTGCATCTTCAAAAGCCTTTGGATTATGCGACGCT	1316
Db	1126	AAGATGGAATAACGAGGGCTCTTAGATTCTTTCAAGGCACTTGTTGATATGCGTCGCT	1185
OY	1317	GCATTCATCATGCGCGTCTTTGCATTCACCTTGCGCCACAGATGATGAGAGAAGGAAGAAA	1376
Db	1186	ACACTCTTCTGCCGCTCTCTCATTTTTCTTGCGCACGAGGGGTCCGAGAACGAAGAAGAGA	1245
OY	1377	TAAATCAAAGCCTTAAGAGACGTCCTTGCAGT---GCACCTAGAGGGGCCAAGAACCGTTA	1433
Db	1246	AAGCCCTAATTTCAAAGAACACCGCTGCAGAAATGTAGCAGGGAGAGATGACACAGTTTA	1305
OY	1434	TCATATCATGATTCAGAGAAAGGGGAAGGTTTGATGATGAGATGCACATTTACCTGAGCTTAG	1493
Db	1306	TCATGTTTTTTGTTAGAGAAAGGCCGGTTTGAAATGGAATCAGTCTTTTGGAGGGGTAA	1365
OY	1494	CAATTTAACTCTGATGATGCTGTGAAGGCTGCTGTTGTTTGAAGTTTCACATCCCTGAATCT	1553
Db	1366	AAGTGTGATCAGGAGAGCTCTAGAAATCTGCAGTGTCTCGCAAGTTCAAGTCTTTAAACA	1425
OY	1554	TGTGCTCTATGGAAGAACTGAAAGGCCCTGAACTTATAGAGGGGGGATGCTTTAAACT	1613
Db	1426	TGAGGCATGTGGGAAGAAAGGCCCTGGAAACTTTAAAGAGAGCAAGAGCTTTAAAT	1485
OY	1614	CTACAAATATATACCCAATTCGCTTGACACAGAGACAAAGCTTTATACCTCAGCTTCAA	1673
Db	1486	ACATGGAATTTACCGCGCTTGCGCTTACGCCAOCAGAGGCTTTGTCAACTTCGAATTTGGA	1545
OY	1674	AGGTGATCTGTAATTTACAGAGTCACTTGAGAGAACATCTTGTCGCAAGTTTGAAGTCAT	1733
Db	1546	GGGAATTCGAGATCTAAATAGTACATTCACAAACAAACCTTGCTGCTAAATTTGAGGTGT	1605
OY	1734	TTTTGTGTAG 1743	
Db	1606	CTTGCTTAG 1615	
RESULT 8			
MTR416755			
LOCUS			
DEFINITION	MTR416755	658 bp mRNA linear PLN 01-NOV-2001	
ACCESSION	AJ416755	Medicago truncatula partial mRNA for alpha1,3-fucosyltransferase (fuct3 gene).	
VERSION	AJ416755.1	GI:16304827	
KEYWORDS	alpha1,3-fucosyltransferase; fuct3 gene.		
SOURCE	ORGANISM	Medicago truncatula	
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.	
REFERENCE	1	Leiter,H., Mucha,J., Staudacher,E., Grimm,R., Glossl,J. and Altmann,F.	
AUTHORS		Purification, cDNA cloning, and expression of GDP-L-Fuc:Asn-linked GlcNAc alpha1,3-fucosyltransferase from mung beans	
JOURNAL		J Biol. Chem. 274 (31), 21830-21839 (1999)	
MEMLINE		99348317	
PUBMED		10419500	
REFERENCE		2 (bases 1 to 658)	
AUTHORS		Afonso,R.	
TITLE		Direct Submission	
JOURNAL		Submitted (15-OCT-2001) Afonso R., Biocologia de celulas Vegetais, Instituto Tecnologia Quimica Biologica, Apartado 127,	
		2780 Oeiras, PORTUGAL	
FEATURES		Location/Qualifiers	
SOURCE		1..658	
		/organism="Medicago truncatula"	
		/isolate="M9/10A"	
		/db_xref="taxon:3880"	
		/clone="BCV 25"	
		/tissue_type="embryogenic callus"	

```

gene
  /country="Portugal"
  2..658
  /gene="fuct3"
  <2..>658
  /gene="fuct3"
  /codon_start=1
  /evidence-experimental
  /product="alpha1,3-fucosyltransferase"
  /protein_id="CAC95159.1"
  /db_xref="GI:16304828"
  /translation="ENNIMARRRGVHIAMTSSIDNPVGYTSMAEYDIMPISPT
  EKAFAPFISNCARNRLOALELLENTNISIDYSGCHNRDRVCLKLTRYKFS
  LAEENSNEEDYVTEKEFQSLVAGTIPVVGPPNIQDPAFSPGSLYIKLEDESVAK
  SMRYLAENPEAYNOSLRMKYEGPSDFKALVDMAVXHSRCRLCIHLAKSREKEKSP
  D"
BASE COUNT      188 a      135 c      149 g      185 t      1 others
ORIGIN
Query Match      24.3%  Score 534;  DB 8;  Length 658;
Best Local Similarity 88.4%;  Pred. No. 4,2e-125;
Matches 579;  Conservative 0;  Mismatches 76;  Indels 0;  Gaps 0;

OY  729  TGAACAATATTTGCCATGGAAGAGGAGGATATACATCGTAATGACACACAGTCT 788
      |||||||
Db   1    TGAACAATATTTGCCATGGAAGAGGAGGATATCAATGCAATGACACACAGTCT 60
      |||||||

OY  789  ATCTTCGATGTCCTGCTGATATTTTTCATGGGCTGATGATGATGACACAGT 848
      |||||
Db   61  ATCATCGACGTCCTGCTGATATTTTTCATGGGCTGATGATGACACAGT 120
      |||||

OY  849  GCAGCCGAAACGTAAGCTGCTTCGACGCTGCTTCATTTCCAAATGCTGCTCGAA 908
      |||||
Db   121  AAGCCGAAACGTAAGCTGCTTCGACGCTGCTTCATTTCCAAATGCTGCTCGAA 180
      |||||

OY  909  TTTCGGTTCGACGCTGTCGAGGCTGGAATAATCAACATCAAAATGATTTGATTC 968
      |||||||
Db   181  TTTCGGTTCGACGCTGTCGAGGCTGGAATAATCAACATCAAAATGATTTGATTC 240
      |||||||

OY  969  TGGTGTTCACAGAACCGTGTATGAGAGAGTGAACAAGTGAAGCCCTGAAGCACTACA 1028
      |||||||
Db   241  TAGTGTTCATGAGATGCTGTATGAGAGAGTGAACAAGTGAAGCCCTGAAGCACTACA 300
      |||||||

OY  1029  ATTTAGCTTACGCTTTGAAATTTGATGAGAAATATGTAACGTAATAATCTTCCA 1088
      |||||||
Db   301  ATTTAGCTTACGCTTTGAAATTTGATGAGAAATATGTAACGTAATAATCTTCCA 360
      |||||||

OY  1089  ATCCCTGTTGCTGGAACGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1148
      |||||||
Db   361  GTCCCTGTTGCTGGAACGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
      |||||||

OY  1149  TCCCTCTCTGCTGCTCAATTTTACATATTAAGAGATAGAGATGTTGAGTCTGTTGCAA 1208
      |||||||
Db   421  TCCCTCTCTGCTGCTCAATTTTATATCAATCAAGAACTGAGATGTTGAGTCTGTTGCAA 480
      |||||||

OY  1209  GACCATGAGATATCTAGCAGAAAATCCGAAAGCATATATATCATATTGAGGTGGAAGTA 1268
      |||||||
Db   481  GTCATGAGATATCTAGCAGAAAATCCGAAAGCATATATATCATATTGAGGTGGAAGTA 540
      |||||||

OY  1269  TGAGGCTCATCTGACTGCTTCAGAGCCCTGAGATATGACAGCTGCTGCTGCTGCTG 1328
      |||||
Db   541  TGAAGGCGCATCTGATCTCTTCAAGGCCCTGCTGATATGACACTGACATCTTCG 600
      |||||

OY  1329  CCGTCTTTCGATTCAGTTGGCCAGAGTGATGAGAGAGAGAGAAATAATATCA 1383
      |||||
Db   601  CCGCTTTTCGATTCAGTTGGCCCTCAAGAGATGAGAGAGAGAGAGAAAGACCCA 655
      |||||

```

```

VERSION          AE277228.1  GI:21628751
KEYWORDS
SOURCE           Arabidopsis thaliana
ORGANISM         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                  Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE        1 (bases 1 to 787)
AUTHORS          Kiefer-Meyer/M.-C., Faye,L. and Gomord,V.
TITLE            Direct Submission
JOURNAL          Submitted (08-JUN-2000) LTI, CNRS UMR 6037, Faculte des Sciences,
                  Universite de Rouen, Mont Saint Aignan 76621, France
FEATURES
  source
    /organism="Arabidopsis thaliana"
    /db_xref="taxon:3702"
    /clone="3W"
    /note="ecotype: WS"
    <1..>787
    /codon_start=2
    /product="alpha 1,3-fucosyltransferase"
    /protein_id="FAM68912.1"
    /db_xref="GI:21628752"
    /translation="STSSSSPSSSEFKKRVSTPLPCVALVIEIGFLRLDNASLVD
    TLTHFFKSSSDLKVGSGIEKCEWELRVDSVYSRDPTDPIFISGNDFKSCVD
    CVMGFTSDKRDPAFGLSHQPTLSIIRSESAQYQENMLAQRKRGYDVMVTSLS
    SDVPVGYSMAEVDIMAPVOPTREELAAAFISNCARNRLOALELMLKTNVKIDSY
    GGCHRNDSGVEVEALKHKFSLAEPENTNEEDYVTEKEFQSLV"
BASE COUNT      202 a      160 c      178 g      247 t
ORIGIN
Query Match      15.9%  Score 349;  DB 8;  Length 787;
Best Local Similarity 73.6%;  Pred. No. 6.4e-78;
Matches 445;  Conservative 0;  Mismatches 160;  Indels 0;  Gaps 0;

OY  493  TCTGAATCGTATTAAGTTGAGGAATGTTGGAGAGGAGATGCTGTCAGCTATTGAGG 552
      |||||
Db   182  TCAGGAATGAGAAATGCGACAGAGTGTAGAGAGAGGATTCAGTACTTATCTAGA 241
      |||||

OY  553  GGCCTTTCAGAGAGCCATTTTGTCTGACGCTGTCGAGTGGAGTGGAACTGCTGTTG 612
      |||||
Db   242  GATTTCATTAAGATCCGATTTTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 301
      |||||

OY  613  GTTGATGTAAATTTGGGTTAGTGGGATGAGAAAGCCAGATGCCGATTTGGTACTCT 672
      |||||
Db   302  GTTGATGTGTAATGGGATTCACATTCAGATTAAGAAACCTGATGGGCTTTGATTAAGT 361
      |||||

OY  673  CAACCACTGGAACAGCTAGCATTCGATGCAATGCAATGCAAGAGAGATATGCTGAG 732
      |||||
Db   362  CATCAACCTGGAAACACATGATATCCGTCATGATGCAATGCAAGAGATATTACCAAGAG 421
      |||||

OY  733  AACATATTTGCTAGGACAGAGAGGAGATTAATCAATCGTAATCAACACAGTCAATCT 792
      |||||
Db   422  AATATCTCTGCTCAAGCAGCAGGAAAGGTTATATATTGATGACACACTAGCTGTCA 481
      |||||

OY  793  TCGATGTTCTGTTGGATATTTTTCATGGGCTGAGATATGATATGATGACACAGTCCAG 852
      |||||
Db   482  TCAATATGTTCTGTTGGATATTTTTCATGGGCGGAATATATATTAATGATGCTCCAGTCAA 541
      |||||

OY  853  CCGAAACTGAGAGCTGCTTGCAGCTGCTTCATTTCCAAATTTGTGTGCTCGAAATTC 912
      |||||
Db   542  CCAAAACAGAGAGAGCTCTGCTGCTGCTTTTTCCAATTCGCGCGCTCGGAATTC 601
      |||||

OY  913  CGTTCGAGCTTTGAGAGCCCTGGAATAATCAAAATCAAAATGATTTGATTTAGTGGT 972
      |||||
Db   602  CGCTGCAAGCTCTTGAAGCTTTATGACAGCATATGTAAGATTTGATTTATGATGGT 661
      |||||

OY  973  TGTACAGAGAAACGATGAGAGAGTGAACAAGTGAAGCCCTGAAGCACTACAAATTT 1032
      |||||
Db   662  TGTACCGGAATTCGAGATGGAGAGTGGAGAGGTTGAAGCTCTTAAGCACTACAAATTC 721
      |||||

OY  1033  AGCTTAGCGTTGAAATTTGAATGAGAGAGATATGTAATGAAATTTCTTCAATCC 1092
      |||||

```

RESULT 9
 AF277228 787 bp mRNA linear PLN 29-JUN-2002
 LOCUS Arabidopsis thaliana clone 3M alpha 1,3-fucosyltransferase mRNA,
 DEFINITION partial cds.
 ACCESSION AF277228

DB	722	AGCTACGCTTTGAGAACACCAAGGAGGATTTATGTCTACAGAGAAGTTCTTCCAACT	781
OY	1093	CTTGT 1097	
Db	782	CTAGT 786	
RESULT 10			
LOCUS	AF277229	588 bp	mRNA linear
DEFINITION	Arabidopsis thaliana clone 1F alpha 1,3-fucosyltransferase mRNA,		
ACCESSION	AF277229		
VERSION	AF277229.1	GI:21628753	
KEYWORDS			
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosids II: Brassicales: Brassicaceae: Arabidopsis. 1 (bases 1 to 588)		
AUTHORS	Kiefer-Meyer/M.-C., Faye/L. and Gomord/V.		
TITLE	Direct Submission		
JOURNAL	Submitted (08-JUN-2000) LIT, CNRS UMR 6037, Faculte des Sciences, Universite de Rouen, Mont Saint Aignan 76821, France		
FEATURES			
source	Location/Qualifiers		
	1..588		
	/organism="Arabidopsis thaliana"		
	/db_xref="taxon:3702"		
	/clone="11F"		
	/note="ecotype: WS"		
	<1..>588		
CDS			
	/codon_start=1		
	/product="alpha 1,3-fucosyltransferase"		
	/protein_id="AA068913.1"		
	/db_xref="GI:21628754"		
	/translation="QEWLEKDYVTSRDTKDPFIISGSKDFSCSVDVCWGFSTDS KRPDAARGLSHQPTGLTIRMESEAQYVOENNLQAQRKGDVMTTSLSDVGVGF SWAPYDIMAPOVPTERKALAAAFISNCARNFRLQALFALMKTVKIDSYGCHRNDD GSVEKVEALKHYKSLAFENMEDYVTEKFFQSLV"		
BASE COUNT	167 a 108 c 137 g 176 t		
ORIGIN			
Query Match	15.7%	Score 346;	DB 8; Length 588;
Best Local Similarity	74.4%;	Pred. No. 3.7e-77;	
Matches 436; Conservative	0;	Mismatches 150;	Indels 0; Gaps 0;
OY	512	AGGAATGGTTGGAGAGGAGAGTGCCTGCACGATATTCGAGGGGCTTTTCCAAAGGCTTA	571
Db	2	AGGAATGGTTGGAGAGGAGAGTGCCTGCACGATATTCGAGAGATTCTACTTAAGATTCCTAAAGATCCGA	61
OY	572	TTTTTGTTCGACCTGATCAGAGTGAAGTGCCTGTCGGTTCGAGTAATAATTTGGAT	631
Db	62	TTTTTATCTCTGTAAGTAACAAGACGCTTCAATGCTGCTCTGTATTTGTATATGGAT	121
OY	632	TTAGTGGGATAGAAAGCCAGATGCCGATTTGGGTTACCTCAACCAAGTGAACAGCTA	691
Db	122	TCACCTTCAGATTAAGAACTGATGGCGCTTTTGGATTAAAGTCATCAACCTGGAACACCTCA	181
OY	632	GCATTCCTCGCATCATGCAATCAGCAATATCTATGCTGAGAACATATTGCCATGGCAA	751
Db	182	GTATATATCCGTTCCATGCAATCAGCAGTATTACCAAGAGCAATATCTGCTCAAGCAC	241
OY	752	GACGAGGGGATATTAACATCGTAATGACAAACAGCTATCTTCGGATTTCTCCTGGAT	811
Db	242	GACGAAAGGATTATGATATTGTGATGACAAACAGCTATCTTCATCAATATCTCCTGGAT	301
OY	812	ATTTTTCATGGGCGAGTATGATATGATGGACCAAGTCCAGCGCAAACTGAAGCTGCTC	871
Db	302	ATTTTTCATGGGCGGATATGATATTATGGGCTCCAGTCCCAACCAAAACAGGAAGCTC	361
OY	872	TTGACGCTGCTTTCATTTCCAAATGTGTGCTCGAAATTTCCGGTTGCAAGCTCTTGAGG	931

LOCUS	AX105537	2069 bp	DNA	Linear	PAT 30-APR-2001
DEFINITION	Sequence 3 from Patent W00125454.				
ACCESSION	AX105537				
VERSION	AX105537.1	GI:13921581			
KEYWORDS					
SOURCE	synthetic construct.				
ORGANISM	artificial construct.				
REFERENCE	artificial sequences.				
AUTHORS	1 (bases 1 to 2069)				
TITLE	V. Zina, L. P. and D'Amour, M. A.				
JOURNAL	Method for regulating transcription of foreign genes in the presence of nitrogen				
	Patent: WO 0125454-A 3 12-APR-2001;				
	Medicago Inc. (CA)				
FEATURES	Location/Qualifiers				
source	1..2069				
	/organism="synthetic construct"				
	/db_xref="taxon:32630"				
	/note="Sequences to be used as promoter for regulating expression of foreign genes"				
BASE COUNT	640 a 389 c 335 g 705 t				
ORIGIN					
Query Match	9.5%	Score 209.4	DB 6	Length 2069;	
Best Local Similarity	66.5%	Pred. No. 2.8e-42;			
Matches 341; Conservative	0;	Mismatches 151;	Indels 21;	Gaps 2;	
Oy 1486	AGGCTAGCAATTTTACCTGTAAGTCTGTAAGGCTGCTGTTGTTGAAGTTCATCC	1545			
Db 170	AGATTCAGCAATTTTACCTGTAAGTCTGTAAGGCTGCTGTTGTTGAAGTTCATCC	229			
Oy 1546	CTGAATCTTGTGCTGTATGGAAGCACTGAAGGCTGGAATTAATGAAGGGGGAGTCT	1605			
Db 230	CTGAATCTTGTGCTGTATGGAAGCACTGAAGGCTGGAATTAATGAAGGGGGAGTAA	289			
Oy 1606	TTAAACCTCTCAAAATTTATCCCAATTTGGCTTTGACACAGACAAGCTTTATACCTTC	1665			
Db 290	TTGAAGGTTTCAAAATTTATCCCTGCGGGCTTGACACAGAGCAAGCTTTATACCTTC	349			
Oy 1666	AGCTTCAAAGTGATGCTGATTTGAGAGTCACTGGAGACAATCCTTGGCCAGTTT	1725			
Db 350	CAGTTCACAGGGGATGTTGATTTTCAAGAGTCACTGGAGAGCAATCCTTGGCCAGTTT	409			
Oy 1726	GAAGTCAATTTTGTGTAGCATGCGCTAA-----ATAGTACTCTGCTTACCTGAAT	1778			
Db 410	GAAGTCAATTTTGTGTAGCATGCGCTAA-----ATAGTACTCTGCTTACCTGAAT	469			
Oy 1779	AGCTTCACCTTACCTGAGCAGTACGCTAGAGTGTGGAATGATGATGCGATGATATGCG	1838			
Db 470	AGCTTCACCTTACCTGAGCAGTACGCTAGAGTGTGGAATGATGATGCGATGATATGCG	529			
Oy 1839	ATGGCTT-----TATTATGCGAGTGTGTTGGCCAAATCATTGATGTTT	1884			
Db 530	ATGGCTTGTGTAATGCTACCTACTTGTGGCCAACTCATGGGGATTTTCAATTCGAAAT	589			
Oy 1885	GTAATAGCATCACACTTAATTTTAACTGTGTTCTGTAGAAAGTCAAAATCCATATTTA	1944			

Db 590 ATACTGCTTCAACCATCTTAACCCCTTTTGTAGATACTGAATGTTCAATTTA 649

Oy 1945 ATGCTTACTTTTAAAGCTCTATCGATCACT 1977

Db 650 ATGTTGGGTTGACTGTTTTTACTTGATTAAT 682

RESULT 12

LOCUS	AX105540	2124 bp	DNA	linear	PAT 30-APR-2001
DEFINITION	Sequence 6 from Patent WO0125454.				
ACCESSION	AX105540				
VERSION	AX105540.1	GI:13921584			

BASE COUNT	ORIGIN
651 a	412 c 339 g 722 t

Query Match	9.5%	Score 209.4	DB 6	Length 2124
Best Local Similarity	66.5%	Pred. No. 2.8e+42		
Matches 341	Conservative	0	Mismatches 151	Indels 21
				Gaps 2

RESULT 13	AX105543	LOCUS	AX105543	2165 bp	DNA	linear	PAT 30-APR-2001
DEFINITION	Sequence	9	from Patent W00125454.				
ACCESSION	AX105543						
VERSION	AX105543.1			GI:13921587			

BASE COUNT	664 a	424 c	345 g	732 t
ORIGIN				

Query Match	9.5%;	Score 209.4;	DB 6;	Length 2165;
Best Local Similarity	66.5%;	Pred. No. 2.8e-42;		
Matches 341; Conservative	0;	Mismatches 151;	Indels 21;	Gaps 2;

Db 590

	LOCUS	AXI05546	2232 bp	DNA	linear	PAT 30-APR-2001
	DEFINITION	Sequence 12 from Patent WO0125454.				
	ACCESSION	AXI05546				
	VERSION	AXI05546.1	GI:13921590			

OY 1945 ATGCTAGTTTACTGCCTTAATCGTCACFCT 1977
 | | | | | | | | | | | | | |
Db 650 ATGTGGCCTTAGTGTTTTACTTGATTAAAT 682
 .

